

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:13:09 ; Search time 50.0148 Seconds  
(without alignments)  
414.909 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTVSFTKGTATYITVNF.....AVDQVKPIALLKFDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/PCUTUS\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	251	1	US-08-425-336-101
2	1277	100.0	251	1	US-08-488-113B-101
3	1277	100.0	251	1	US-08-477-484B-101
4	1277	100.0	251	1	US-08-646-360-101
5	1277	100.0	251	2	US-08-839-765-101
6	1277	100.0	251	2	US-09-136-389-101
7	1277	100.0	251	2	US-09-610-838-101
8	1277	100.0	251	2	US-09-711-485-101
9	1273	99.7	251	1	US-08-425-336-99
10	1273	99.7	251	1	US-08-488-113B-99
11	1273	99.7	251	1	US-08-477-484B-99
12	1273	99.7	251	1	US-08-646-360-99
13	1273	99.7	251	1	US-08-839-765-99
14	1273	99.7	251	2	US-08-839-765-100
15	1273	99.7	251	2	US-09-136-389-100
16	1273	99.7	251	2	US-09-610-838-100
17	1273	99.7	251	2	US-09-711-485-100
18	1273	99.7	251	2	US-09-136-389-99
19	1273	99.7	251	2	US-09-610-838-99
20	1273	99.7	251	2	US-09-711-485-99
21	1273	99.7	251	2	US-09-136-389-100
22	1273	99.7	251	2	US-09-610-838-100
23	1273	99.7	251	2	US-09-711-485-100
24	1273	99.7	251	2	US-09-136-389-100
25	1269	99.4	251	1	US-08-425-336-2
26	1269	99.4	251	1	US-08-488-113B-2
27	1269	99.4	251	1	US-08-477-484B-2

28	1269	99.4	251	1	US-08-488-113B-110	Sequence 110, App
29	1269	99.4	251	1	US-08-477-484B-2	Sequence 2, Appli
30	1269	99.4	251	1	US-08-477-484B-110	Sequence 110, App
31	1269	99.4	251	1	US-08-646-360-2	Sequence 2, Appli
32	1269	99.4	251	1	US-08-646-360-110	Sequence 110, App
33	1269	99.4	251	1	US-08-621-803-247	Sequence 247, App
34	1269	99.4	251	2	US-08-839-765-2	Sequence 2, Appli
35	1269	99.4	251	2	US-08-839-765-110	Sequence 110, App
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37	1269	99.4	251	2	US-09-136-389-110	Sequence 110, App
38	1269	99.4	251	2	US-09-217-352-247	Sequence 247, App
39	1269	99.4	251	2	US-09-610-838-2	Sequence 2, Appli
40	1269	99.4	251	2	US-09-610-838-110	Sequence 110, App
41	1269	99.4	251	2	US-09-711-485-2	Sequence 2, Appli
42	1269	99.4	251	2	US-09-711-485-110	Sequence 110, App
43	1269	99.4	251	2	US-09-645-603B-2	Sequence 2, Appli
44	1266	99.1	251	1	US-07-901-707-2	Sequence 2, Appli
45	1266	99.1	251	1	US-07-988-430-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-425-336-101

; Sequence 101, Application US/08425336

; Patent No. 5621083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen P.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; TITLE OF INVENTION: Proteins

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/425,336

; APPLICATION NUMBER: US/08/425,336

; FILING DATE: 18-APR-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Thomas C.

; REGISTRATION NUMBER: P-36,989

; REFERENCE/DOCKET NUMBER: 31394

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 101:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 251 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-425-336-101

Query Match	100.0%	Score 1277;	DB 1;	Length 251;
Best Local Similarity	100.0%;	Pred. No. 9.8e-119;		
Matches 251;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	GLDVSFSTKGATVITTVNFLELRVVKLKEPENGSHGIPLLRKKADDPKAFVLVALSNDN	60	
Qy	61	GQLAEIAIDVTSVVVGVQVVRNSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLGEK	120	
Db	61	GQLAEIAIDVTSVVVGVQVVRNSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLGEK	120	
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Db	121	AYRETTDLGIEPLRIGIKKL DENAIDNYKPTETIASLLVVIQWYSEARPTFIENQIRNN	180	
Qy	181	FQQRIRPANNITISLENWKGLKSFQIRTS GANGMPSEAVELERANGKKYVYTVAVDQVKPKI	240	
Db	181	FQQRIRPANNITISLENWKGLKSFQIRTS GANGMPSEAVELERANGKKYVYTVAVDQVKPKI	240	
Qy	241	ALLKFVDKPK	251	
Db	241	ALLKFVDKPK	251	

RESULT 2  
US-08-488-113B-101  
; Sequence 101, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:

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/ TELEPHONE: 312/707-8889
/
/ TELEFAX: 312/707-9155
/
/ TELEX: 650 388-1248
/
/ INFORMATION FOR SEQ ID NO: 101:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 251 amino acids
/
/ TYPE: amino acid
/
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: protein
/
US-08-488-113B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GLDVSFSTKGATVITVNFNLRLVKLKPEGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60
DB 1 GLDVSFSTKGATVITVNFNLRLVKLKPEGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60
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DB 61 GQLAEIAIDVTSVVVGVYQVRNRSYFFKQADPADAAEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AVRETTDLGIETPLRIGIKLDENAINDKTEIASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AVRETTDLGIETPLRIGIKLDENAINDKTEIASSLLVVIQMVSEAAARFTFIENQIRNN 180
QY 181 FQOIRIPANNITISLENKWKLSFOIRTSYGANGMPSEAVELERANGKKYVYTVAVDOVKPKI 240
DB 181 FQOIRIPANNITISLENKWKLSFOIRTSYGANGMPSEAVELERANGKKYVYTVAVDOVKPKI 240
QY 241 ALIKFVDKDPK 251
DB 241 ALIKFVDKDPK 251

RESULT 3
US-08-477-484B-101
/ Sequence 101, Application US/08477484B
/ Patent No. 5756699
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Better, Marc D.
/
/ APPLICANT: Carroll, Stephen F.
/
/ APPLICANT: Studnika, Gary M.
/
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/
/ TITLE OF INVENTION: Proteins
/
/ NUMBER OF SEQUENCES: 169
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/
/ STREET: 500 West Madison Street, 34th floor
/
/ CITY: Chicago
/
/ STATE: Illinois
/
/ COUNTRY: USA
/
/ ZIP: 60661
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/477,484B
/
/ FILING DATE: 07-JUN-1995
/
/ CLASSIFICATION: 530
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 08/425,336
/
/ FILING DATE: 18-APR-1995
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 08/064,691
/
/ FILING DATE: 12-MAY-1993
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 07/988,430
/
/ FILING DATE: 09-DEC-1992
/
/ PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; FILING DATE: 12-MAY-1993
; NAME: McNicholas, Janet M.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAPVLVNSNDN 60
Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAPVLVNSNDN 60
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Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENADIDNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADIDNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
Qy 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Db 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 4
US-08-646-360-101
; Sequence 101, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-360-101

Query Match 100.0%; Score 1277; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAPVLVNSNDN 60
Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHGIPLLRKADDPGKAPVLVNSNDN 60
Qy 61 GQLAEIAIDVTSVYVGVQVRNRSYFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120
Db 61 GQLAEIAIDVTSVYVGVQVRNRSYFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120
Qy 121 AYRETTDLGIEPLRIGIKKLDENADIDNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKKLDENADIDNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
Qy 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Db 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVRPKI 240
Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 5
US-08-839-765-101
; Sequence 101, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

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; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-839-765-101

Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred.No.9.e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTSVSTGATYITVNFNLRLVKLKPEGNSHGIPLLRKKADDPGKAPVLVALSNDN 60
Db |||||
Qy 1 GLDTSVSTGATYITVNFNLRLVKLKPEGNSHGIPLLRKKADDPGKAPVLVALSNDN 60
Db |||||

Qy 61 GOLAEIAIDVTSVVVGQYQVRNRSYFPKADPADAAEGLFKNTIKTRLHFGGSYPSLGEK 120
Db |||||
Qy 61 GOLAEIAIDVTSVVVGQYQVRNRSYFPKADPADAAEGLFKNTIKTRLHFGGSYPSLGEK 120
Db |||||

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIDNXYKTEIASLLWVQMVSAAARFTFIENQIRNN 180
Db |||||
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIDNXYKTEIASLLWVQMVSAAARFTFIENQIRNN 180
Db |||||

Qy 181 FQOIRPANNTISLENKWKLSFOIRTSANGMPSEAVELERANGKYYVTVAVDQVQPKI 240
Db |||||
Qy 181 FQOIRPANNTISLENKWKLSFOIRTSANGMPSEAVELERANGKYYVTVAVDQVQPKI 240
Db |||||

Qy 241 ALLKFVDKDKP 251
Db |||||
Qy 241 ALLKFVDKDKP 251
Db |||||

RESULT 6
US-09-136-389-101
; Sequence 101, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

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Qy 241 ALLKFDKDPK 251  
Db 241 ALLKFDKDPK 251

RESULT 7  
US-09-610-838-101  
; Sequence 101, Application US/09610838  
; Patent No. 6376217  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/610,838  
; FILING DATE: 06-JUL-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/136,389  
; FILING DATE: 18-AUG-1998  
; APPLICATION NUMBER: 08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-610-838-101

Query Match 100.0%; Score 1277; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 9.8e-119;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATVITYYVNFLELVKLPKPGNSHGIPLLRKKADDPGKAPVLVALSNDN 60  
Db 61 GOLAEIAIDVTSVVVGVQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
Db 61 GOLAEIAIDVTSVVVGVQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASSLLVVIQWVSEAAARPTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASSLLVVIQWVSEAAARPTFIENQIRNN 180  
Qy 181 FOORIRPANTTISLENKWKGLSFOIRTSANGMPSEAVELERANGKYYVTVAVDQVVKPKI 240  
Db 181 FOORIRPANTTISLENKWKGLSFOIRTSANGMPSEAVELERANGKYYVTVAVDQVVKPKI 240  
Qy 241 ALLKFDKDPK 251  
Db 241 ALLKFDKDPK 251

RESULT 8  
US-09-711-485-101  
; Sequence 101, Application US/09711485  
; Patent No. 6649742  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/711,485  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/839,765  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-711-485-101

Query Match      100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.8e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60
Db 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60

Qy 61 GOLAEIAIDVTSVVVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVVVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 9
US-08-425-336-99
; Sequence 99, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-0448
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 99:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-99

Query Match      99.7%; Score 1273; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 2.5e-118;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60
Db 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPGKAPVLVALSNDN 60

Qy 61 GOLAEIAIDVTSVVVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
Db 61 GOLAEIAIDVTSVVVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
Db 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFVDKDPK 251
Db 241 ALLKFVDKDPK 251

RESULT 10
US-08-425-336-100
; Sequence 100, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-6300
; TELEPHONE: 312/474-6300
```

TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-100

Query Match 99.7%; Score 1273; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-118;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVSLNDN 60  
Db 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVSLNDN 60  
Qy 61 GQLAEIAIDVTSVYVGVQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120  
Db 61 GQLAEIAIDVTSVYVGVQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120  
Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180  
Qy 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Qy 241 ALLKFVDKDPK 251  
Db 241 ALLKFVDKDPK 251

## RESULT 11

US-08-488-113B-99  
Sequence 99, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-118;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVSLNDN 60  
Db 1 GLDTSFSTKGATITVYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVSLNDN 60  
Qy 61 GQLAEIAIDVTSVYVGVQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120  
Db 61 GQLAEIAIDVTSVYVGVQVNRNRSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120  
Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180  
Qy 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Qy 241 ALLKFVDKDPK 251  
Db 241 ALLKFVDKDPK 251

## RESULT 12

US-08-488-113B-100  
Sequence 100, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-118;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVSLNDN 60  
Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVSLNDN 60

Qy 61 GOLAEIAIDVTSVYVGVQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120  
Db 61 GOLAEIAIDVTSVYVGVQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPEIASSLLVLIQVSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPEIASSLLVLIQVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFDVKDPK 251  
Db 241 ALLKFDVKDPK 251

RESULT 13  
US-08-477-484B-99  
Sequence 99, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESS: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-99

Query Match 99.7%; Score 1273; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-118;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVSLNDN 60  
Db 1 GLDVSFSTKGATITVYVFNELRVKLPKGNHSHGIPLLRKKADDPGKAFVLVSLNDN 60

Qy 61 GOLAEIAIDVTSVYVGVQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120  
Db 61 GOLAEIAIDVTSVYVGVQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120

Qy 121 AYRETTDLGIEPLRIGIKKLDENADNYKPEIASSLLVLIQVSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADNYKPEIASSLLVLIQVSEAAARFTFIENQIRNN 180

Qy 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

Qy 241 ALLKFDVKDPK 251  
Db 241 ALLKFDVKDPK 251

RESULT 14  
US-08-477-484B-100  
Sequence 100, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
;; TITLE OF INVENTION: Proteins  
;; NUMBER OF SEQUENCES: 169  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
;; STREET: 500 West Madison Street, 34th floor  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60661  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/477,484B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/425,336  
;; FILING DATE: 18-APR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/064,691  
;; FILING DATE: 12-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/988,430  
;; FILING DATE: 09-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C3A  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 100:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 251 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-477-484B-100

Query Match 99.7%; Score 1273; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-118;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GLDVSFSTGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60  
Db 1 GLDVSFSTGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60  
Qy 61 GOLAEIAIDVTSVVGQVQRNRSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Db 61 GOLAEIAIDVTSVVGQVQRNRSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Qy 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180  
Qy 181 PQQIRPANNITISLENKWKLSFQIRTSANGMFSSEAVELERANGKKYVTVAVDQVKPKI 240  
Db 181 PQQIRPANNITISLENKWKLSFQIRTSANGMFSSEAVELERANGKKYVTVAVDQVKPKI 240  
Qy 241 ALLKFEVDKPK 251  
Db 241 ALLKFEVDKPK 251

## RESULT 15

US-08-646-360-99  
; Sequence 99, Application US/08646360  
; Patent No. 5837491  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-646-360-99  
Query Match 99.7%; Score 1273; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-118;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GLDVSFSTGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60  
Db 1 GLDVSFSTGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVNSDN 60  
Qy 61 GOLAEIAIDVTSVVGQVQRNRSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Db 61 GOLAEIAIDVTSVVGQVQRNRSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Qy 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180

Db	121	AYRETTDLGIEPLRIGIKKLDENALDNYKPTETIASSLLVVIQWSEARFTFIENQIRNN	180
Qy	181	FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELEBRANGKYYVTAVDQVKPKI	240
Db	181	FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELEBRANGKYYVTAVDQVKPKI	240
Qy	241	ALLKFVDKDPK	251
Db	241	ALLKFVDKDPK	251

Search completed: February 10, 2006, 10:15:59  
Job time : 51.0148 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 212.1 Seconds  
(without alignments)  
834.927 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTVSFTKATYTYNF.....AVDQVKPKALLKFDKDPK 251

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	316	1	RIPG_GELMU
2	1242.5	96.5	258	2	Q9S9E4_GELMU
3	394.5	30.7	581	2	Q94BW5_CINCA
4	393.5	30.6	580	2	Q94BW3_CINCA
5	392.5	30.5	549	2	Q9FV22_CINCA
6	388	30.1	299	2	Q8GZNS_9ROSI
7	386.5	30.0	580	2	Q94BW4_CINCA
8	361.5	28.1	563	2	Q8GT32_SAMNI
9	357.5	27.8	297	2	Q8GZP0_9ROSI
10	352	27.4	563	1	NTGB_SAMNI
11	352	27.4	563	2	Q945S2_SAMNI
12	348.5	27.1	563	2	Q04367_SAMNI
13	346	26.9	264	2	Q684J5_MOMCH
14	346	26.9	286	1	RIP2_MOMBA
15	346	26.9	286	1	RIP3_MOMCH
16	346	26.9	286	1	QSPZ05_MOMCH
17	344	26.7	541	2	Q41174_RICCO
18	343	26.7	576	1	RICI_RICCO
19	341.5	26.5	265	1	RIP2_PHYDI
20	338.5	26.3	294	1	RIP1_TRIAN
21	337.5	26.2	564	2	Q9AVR2_9DIPS
22	334.5	26.0	564	1	AGGL_RICCO
23	333.5	25.9	527	1	ABRB_ABRPR
24	333	25.9	282	1	RIP2_BRYDI
25	330.5	25.7	294	1	RIPA_PHYAM
26	329	25.6	252	2	Q38760_ABRPR
27	327.5	25.4	293	2	Q8VYU0_9ROSI
28	327.5	25.4	294	2	Q8H1W1_PHYAM
29	325.5	25.3	275	2	Q84LJ1_GYNPE
30	325	25.3	313	1	RIP1_PHYAM
31	325	25.3	313	2	Q6PWU4_PHYAM

32	325	25.3	313	2	Q53YN2_PHYAM	Q53yn2 phytolacca
33	324.5	25.2	277	2	Q84JRI_GYNPE	Q84jri gynostemma
34	324.5	25.2	293	2	Q89452_9ROSI	Q89452 jatropa cu
35	324	25.2	289	2	Q41216_TRIKI	Q41216 trichosan
36	323.5	25.1	277	2	Q8GV09_GYNPE	Q8gv09 gynostemma
37	322.5	25.1	275	2	Q8H1Y4_GYNPE	Q8h1y4 gynostemma
38	322.5	25.1	298	2	Q5F013_GYNPE	Q5f013 gynostemma
39	321	24.9	289	1	RIP1_TRIKI	P09989 trichosan
40	321	24.9	289	2	Q94KE4_TRIKI	Q94ke4 trichosan
41	321	24.9	567	2	Q6H267_VISAL	Q6h267 visum albu
42	320.5	24.9	277	2	Q8GV11_GYNPE	Q8gv11 gynostemma
43	320.5	24.9	565	2	Q04071_SAMNI	Q04071 sambucus ni
44	320	24.9	251	2	Q7DM12_ABRPR	Q7dm12 abrus preca
45	320	24.9	252	2	Q38761_ABRPR	Q38761 abrus preca

#### ALIGNMENTS

#### RESULT 1

ID RIPG\_GELMU STANDARD; PRT; 316 AA.  
AC P33186;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase).  
GN Name=GEL;  
OS Gelonium multiflorum (Euphorbiaceae himalaya).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosid; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;  
OC Geloneae; Gelonium.  
OX NCBI\_TaxID=3379;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M; Nolan P.A., Garrison D.A., Better M.;  
RA "Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein from Gelonium multiflorum.";  
RL Gene 134:223-227(1993).  
RN [2]  
RP PROTEIN SEQUENCE OF 47-93.  
RC TISSUE=Seed;  
RX MEDLINE=89326691; PubMed=2753596;  
RA Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.;  
RT "N-terminal sequence of some ribosome-inactivating proteins.";  
RL Int. J. Pept. Protein Res. 33:263-267(1989).  
RN [3]  
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
RP MEDLINE=95333189; PubMed=7608981;  
RA Hosur M.V., Nair B., Satyamurthy P., Misquith S., Surolia A., Kannan K.K.;  
RT "X-ray structure of gelonin at 1.8-A resolution.";  
RL J. Mol. Biol. 250:368-380(1995).  
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
CC -|- SUBUNIT: Homodimer.  
CC -|- SIMILARITY: Belongs to the ribosome-inactivating protein family.  
CC Type 1 RIP subfamily.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; L12243; AAA16312.1; -; mRNA.

PIR; JT0753; JT0753.

HSSP; P09989; 1MRJ.

InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;  
KW Protein synthesis inhibitor; Signal; Toxin.  
FT SIGNAL 1 26 Potential.  
FT PROPEP 27 46  
FT CHAIN 47 297 Ribosome-inactivating protein gelonin.  
FT PROPEP 298 316 Removed in mature form.  
FT ACT SITE 212 212  
FT CARBOHYD 235 235 N-linked (GlcNAc. . .).  
FT DISULFID 90 96 C -> K (in Ref. 2).  
FT CONFLICT 90 90 P -> D (in Ref. 2).  
FT CONFLICT 93 93  
SQ SEQUENCE 316 AA; 35419 MW; 1252F3E710901B85 CRC64;  
  
Query Match 100.0%; Score 1287; DB 1; Length 316;  
Best Local Similarity 100.0%; Pred. No. 5.3e-100;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GLDTVSFSTKGATITTYVNFNLRLVVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60  
47 GLDTVSFSTKGATITTYVNFNLRLVVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 106  
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGS 120  
107 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGS 166  
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQVSEAAARFTFENQIRNN 180  
167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQVSEAAARFTFENQIRNN 226  
QY 181 FOQIRPNNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 240  
227 FOQIRPNNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 286  
QY 241 ALLKFVDKDPK 251  
DB 287 ALLKFVDKDPK 297  
  
RESULT 2  
Q9S9B4 GELMU  
ID Q9S9E4\_GELMU PRELIMINARY; PRT; 258 AA.  
AC Q9S9E4;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE rRNA -glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).  
OS Gelonium multiflorum (Euphorbiaceae himalay).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;  
OC Gelsoniae; Gelonium.  
OX NCBI\_TaxID=3979;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=96006751; PubMed=7553224;  
RA Rosenthal M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,  
RA Toman P.D., Cheung L.;  
RT Amino acid sequence analysis, gene construction, cloning, and  
RT expression of Gelonin, a toxin derived from Gelonium multiflorum.";  
RL J. Interferon Cytokine Res. 15:547-555 (1995).  
DR HSP; P09989; 1MRJ.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0037148; P:negative regulation of protein biosynthesis; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.  
SQ SEQUENCE 258 AA; 28826 MW; 13D688673F4D6B06 CRC64;  
  
Query Match 96.5%; Score 1242.5; DB 2; Length 258;  
Best Local Similarity 95.8%; Pred. No. 2.3e-96;  
Matches 248; Conservative 1; Mismatches 1; Indels 9; Gaps 2;  
  
QY 1 GLDTVSFSTKGATITTYVNFNLRLVVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60  
DB 1 GLDTVSFSTKGATITTYVNFNLRLVVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 59  
QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGS 112  
60 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGS 119  
QY 113 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQVSEAAARFTF 172  
120 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQVSEAAARFTF 179  
QY 173 IENQIRPNNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 232  
180 IENQIRPNNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 239  
QY 233 VDQVKPKIALIKFVDKDPK 251  
DB 240 VDQVKPKIALIKFVDKDPK 258  
  
RESULT 3  
Q94BW5 CINCA  
ID Q94BW5\_CINCA PRELIMINARY; PRT; 581 AA.  
AC Q94BW5;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Type 2 ribosome-inactivating protein cinnamomin I precursor.  
OS Cinnamomum camphora (Camphor tree).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;  
OC Cinnamomum.  
OX NCBI\_TaxID=13429;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;  
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;  
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated  
RT from the seeds of camphor tree and their expression patterns.";  
RL Gene 284:215-223 (2002).  
DR EMBL; AY039801; AAK82458.1; -; Genomic\_DNA.  
DR HSP; P02879; 2AAI  
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00652; Ricin\_B\_lectin; 2.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR SMART; SM00458; RICIN; 2.  
DR PROSITE; PS02031; RICIN\_B\_LECTIN; 2.  
KW SIGNAL.  
FT SIGNAL 1 32 Potential.  
FT CHAIN 33 581 type 2 ribosome-inactivating protein  
FT cinnamomin I.  
SQ SEQUENCE 581 AA; 64215 MW; 688F5F8FEA3D196 CRC64;  
  
Query Match 30.7%; Score 394.5; DB 2; Length 581;  
Best Local Similarity 39.7%; Pred. No. 1.8e-24;  
Matches 100; Conservative 45; Mismatches 94; Indels 13; Gaps 8;  
  
QY 4 TVSFSTKGATITTYVNFNLRLVVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 59  
35 TVTFSTKATKTSYTFQTFEALRAQLASGEHPGVPMRERSTVPDSKRFILVELSNWAAD 94



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Qy 60 NGQLAEIAIDVTSVVVGVYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGSGYPSLEG 118
Db 95 SP--VTLAVDVNAYVAYRTGQSFFLRDNPDPAIENLLPDKRYTFPPSGSYTDLEG 152
Qy 119 EKA-YRETTDLGIEPLRIGIKKLDENADINYKPTETAIASSLLVVIQMVSEAAARFTFIENQI 177
Db 153 VAGERREILLGMDPLENAISALWISNLNQOR--ALARSLIVVIQMVAEAVRFRFIEYRV 210
Qy 178 RNNFO--QRIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAV-D 234
Db 211 RGSISRAEMFRPDPAMLSLENKWSALSNAVQSQGGVFSFVPELRSISNKPVTYVGSVSD 270
Qy 235 QVKPKIALLKVF 246
Db 271 RVISGLAIMLFI 282

RESULT 4
Q94BW3 CINCA
ID Q94BW3 CINCA PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xie L., Liu R.S., Gong Z.Z., Liu W.Y.;
RL MEDLINE=2188636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated
RT from the seeds of camphor tree and their expression patterns. ";
RL Gene 284:215-223(2002).
DR EMBL; AY039803; AAK82460.1; -; Genomic_DNA.
DR HSSP; P02879; 2AAL.
DR GO; GO:0030598; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match 30.6%; Score 393.5; DB 2; Length 580;
Best Local Similarity 39.8%; Pred. No. 2.2e-24;
Matches 101; Conservative 46; Mismatches 90; Indels 17; Gaps 9;

Qy 4 TVSFSTKATYITVYVFNELRVKLPKGNHSHGIPLLRKKCDP-GKCFVLVALSN---D 59
Db 35 TVTFTTKATKTSYTOFIEALRAQLASGEEPHGIPVWRERSTVPDSKRFFILVELSNWAAD 94
Qy 60 NGQLAEIAIDVTSVVVGVYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGSGYPSLE- 117
Db 95 SP--VTLAVDVNAYVAYRTGQSFFLRDNPDPAIENLLPDKRYTFPPSGSYTDLER 152
Qy 118 --GEKAYRETTDLGIEPLRIGIKKLDENADINYKPTETAIASSLLVVIQMVSEAAARFTFIEN 175
Db 153 VAGER--REELLGMDPLENAISALWISNLNQOR--ALARSLIVVIQMVAEAVRFRFIEY 208
Qy 176 QIRNFP--QRIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAV 233
Db 209 RVRESITRAEMFRPDPAMLSLENKWSALSNAVQSQGGVFSFVPELRSISNKPVTYVGSV 268

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Qy 234 -DOVKPKIALLKVF 246
Db 269 SDRVISGLAIMLFI 282

RESULT 5
Q9FV22 CINCA
ID Q9FV22 CINCA PRELIMINARY; PRT; 549 AA.
AC Q9FV22;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin (fragment).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
OC Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xie L., Liu W.Y., Wang E.-D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259548; AAF68978.2; -; mRNA.
DR HSSP; P02879; 2AAL.
DR GO; GO:0030598; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR PRINTS; PR00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON_TER
SQ SEQUENCE 549 AA; 60648 MW; 02607FB607CA44B0 CRC64;

Query Match 30.5%; Score 392.5; DB 2; Length 549;
Best Local Similarity 39.7%; Pred. No. 2.5e-24;
Matches 100; Conservative 45; Mismatches 94; Indels 13; Gaps 8;

Qy 4 TVSFSTKATYITVYVFNELRVKLPKGNHSHGIPLLRKKCDP-GKCFVLVALSN---D 59
Db 3 TVTFTTKATKTSYTOFIEALRAQLASGEEPHGIPVWRERSTVPDSKRFFILVELSNWAAD 62
Qy 60 NGQLAEIAIDVTSVVVGVYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGSGYPSLEG 118
Db 63 SP--VTLAVDVNAYVAYRTGQSFFLRDNPDPAIENLLPDKRYTFPPSGSYTDLEG 120
Qy 119 EKA-YRETTDLGIEPLRIGIKKLDENADINYKPTETAIASSLLVVIQMVSEAAARFTFIENQI 177
Db 121 VAGERREILLGMDPLENAISALWISNLNQOR--ALARSLIVVIQMVAEAVRFRFIEYRV 178
Qy 178 RNNFO--QRIRPANNITISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAV-D 234
Db 179 RGSISRAEMFRPDPAMLSLENKWSALSNAVQSQGGVFSFVPELRSISNKPVTYVGSVSD 238
Qy 235 QVKPKIALLKVF 246
Db 239 RVISGLAIMLFI 250

RESULT 6
Q8GZN9 GROS
ID Q8GZN9 GROS PRELIMINARY; PRT; 299 AA.
AC Q8GZN9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ribosome inactivating protein Eueerratin 2 precursor
DE (EC 3.2.2.22).
GN Name=Eus2;
OS Euphorbia serrata.

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[illegible]





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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1287	100.0	251	1	US-08-425-336-2	Sequence 2, Appli
2	1287	100.0	251	1	US-08-488-113B-2	Sequence 2, Appli
3	1287	100.0	251	1	US-08-477-484B-2	Sequence 2, Appli
4	1287	100.0	251	1	US-08-646-360-2	Sequence 2, Appli
5	1287	100.0	251	1	US-08-621-803-247	Sequence 247, App
6	1287	100.0	251	2	US-08-839-765-2	Sequence 2, Appli
7	1287	100.0	251	2	US-09-136-389-2	Sequence 2, Appli
8	1287	100.0	251	2	US-09-217-352-247	Sequence 247, App
9	1287	100.0	251	2	US-09-610-838-2	Sequence 2, Appli
10	1287	100.0	251	2	US-09-711-485-2	Sequence 2, Appli
11	1287	100.0	251	2	US-09-645-603B-2	Sequence 2, Appli
12	1284	99.8	251	1	US-07-901-707-2	Sequence 2, Appli
13	1284	99.8	251	1	US-07-988-430-2	Sequence 2, Appli
14	1284	99.8	251	4	PCR-US92-09487-2	Sequence 2, Appli
15	1284	99.8	293	1	US-08-621-803-259	Sequence 259, App
16	1284	99.8	293	2	US-09-217-352-259	Sequence 259, App
17	1284	99.8	309	1	US-08-621-803-253	Sequence 253, App
18	1284	99.8	309	2	US-09-217-352-253	Sequence 253, App
19	1284	99.8	332	1	US-08-621-803-251	Sequence 251, App
20	1284	99.8	332	2	US-09-217-352-251	Sequence 251, App
21	1282	99.6	251	1	US-08-425-336-108	Sequence 108, App
22	1282	99.6	251	1	US-08-488-113B-108	Sequence 108, App
23	1282	99.6	251	1	US-08-477-484B-108	Sequence 108, App
24	1282	99.6	251	1	US-08-646-360-108	Sequence 108, App
25	1282	99.6	251	2	US-08-839-765-108	Sequence 108, App
26	1282	99.6	251	2	US-09-136-389-108	Sequence 108, App
27	1282	99.6	251	2	US-09-610-838-108	Sequence 108, App

Query Match 100.0%; Score 1287; DB 1; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.2e-124; Mismatches 0; Gaps 0;  
Matches 251; Conservative 0; Indels 0; Gaps 0;  
  
QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
  
QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
  
QY 121 AYRETTDLGIEPLRIGIKLDENADINYPTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKLDENADINYPTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
  
QY 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

## RESULT 2

US-08-488-113B-2  
; Sequence 2, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-488-113B-2

Query Match 100.0%; Score 1287; DB 1; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.2e-124; Mismatches 0; Gaps 0;  
Matches 251; Conservative 0; Indels 0; Gaps 0;  
  
QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
  
QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
  
QY 121 AYRETTDLGIEPLRIGIKLDENADINYPTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKLDENADINYPTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
  
QY 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

## RESULT 3

US-08-477-484B-2  
; Sequence 2, Application US/08477484B  
; Patent No. 5756699  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,484B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-2

Query Match 100.0%; Score 1287; DB 1; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.2e-124;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWVSEAAARFTFIENQIRNN 180  
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 4  
US-08-646-360-2  
Sequence 2, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen P.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-2

Query Match 100.0%; Score 1287; DB 1; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.2e-124;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASLLVVIQWVSEAAARFTFIENQIRNN 180  
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 5  
US-08-621-803-247  
Sequence 247, Application US/08621803  
Patent No. 5851802  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-621-803-247

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Query Match      100.0%; Score 1287; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITVYVNFLELRVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITVYVNFLELRVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

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## RESULT 6

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US-08-839-765-2
; Sequence 2, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765

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; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-2

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Query Match      100.0%; Score 1287; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.2e-124;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITVYVNFLELRVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60
DB 1 GLDVSFSTKGATITVYVNFLELRVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIQWSEAAARFTFIENQIRNN 180

QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240
DB 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVADVQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

```

## RESULT 7

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US-09-136-389-2
; Sequence 2, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago

```

STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE: 09/09/136,389

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70.P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-136-389-2

Query Match 100.0%; Score 1287; DB 2; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-124; Mismatches 0; Indels 0; Gaps 0;  
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVNSDN 60  
 DB 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVNSDN 60  
 QY 61 QGLAIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120  
 DB 61 QGLAIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIOMVSEAAARFTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIOMVSEAAARFTFIENQIRNN 180  
 QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 8  
 US-09-217-352-247  
 ; Sequence 247, Application US/09217352

Patent No. 6274344  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
 NUMBER OF SEQUENCES: 265  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/217,352  
 FILING DATE: 09/09/217,352

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/621,803  
 FILING DATE: 22-MAR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 REFERENCE/DOCKET NUMBER: 27129/33199  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 247:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-217-352-247

Query Match 100.0%; Score 1287; DB 2; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-124; Mismatches 0; Indels 0; Gaps 0;  
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVNSDN 60  
 QY 61 QGLAIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120  
 DB 61 QGLAIAIDVTSVYVGVQVNRYSFFKADPDAAYEGLFKNTIKTRLHFGGSPSLEGEK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIOMVSEAAARFTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASSLLVVIOMVSEAAARFTFIENQIRNN 180  
 QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 9  
 US-09-610-838-2  
 ; Sequence 2, Application US/09610838  
 ; Patent No. 6376217  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnika, Gary M.

```

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-2
;
; Query Match 100.0%; Score 1287; DB 2; Length 251;
; Best Local Similarity 100.0%; Pred. No. 1.2e-124;
; Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GLDTSVSTKGTATITVYVFNELRVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
Db 1 GLDTSVSTKGTATITVYVFNELRVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
;
Qy 61 GQLAEIAIDVTSVVVGQVNRNRYFFKDAADAAVEGLFKNTIKTRLHFGGSYPSEGEK 120
Db 61 GQLAEIAIDVTSVVVGQVNRNRYFFKDAADAAVEGLFKNTIKTRLHFGGSYPSEGEK 120
;
Qy 121 AYRETTDLGIEPLRIGIKLDENADNPKPTIASLLVVIQWSEARFTPIENQIRNN 180
Db 121 AYRETTDLGIEPLRIGIKLDENADNPKPTIASLLVVIQWSEARFTPIENQIRNN 180
;
Qy 181 FOQRIIPANNITISLENKWKLSFQIRTSANGMFSEAVELEIRANGKYYVTVADQVKPKI 240
Db 181 FOQRIIPANNITISLENKWKLSFQIRTSANGMFSEAVELEIRANGKYYVTVADQVKPKI 240

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Qy 241 ALLKRFVDKDPK 251
Db 241 ALLKRFVDKDPK 251
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RESULT 10
US-09-711-485-2
; Sequence 2, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-711-485-2
;
; Query Match 100.0%; Score 1287; DB 2; Length 251;
; Best Local Similarity 100.0%; Pred. No. 1.2e-124;
; Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GLDTSVSTKGTATITVYVFNELRVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60
;
Qy 61 GQLAEIAIDVTSVVVGQVNRNRYFFKDAADAAVEGLFKNTIKTRLHFGGSYPSEGEK 120

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Db 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
Db 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
Db 241 ALLKFVDKDPK 251

RESULT 11  
US-09-645-603B-2  
; Sequence 2, Application US/09645603B  
; Patent No. 6652861  
; GENERAL INFORMATION:  
; APPLICANT: LEE-HUANG, Sylvia  
; TITLE OF INVENTION: Anti-HIV and Anti-tumor Peptides and Truncated Polypeptides of  
; FILE REFERENCE: LEE-HUANG 4A  
; CURRENT APPLICATION NUMBER: US/09/645,603B  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/150,885  
; PRIOR FILING DATE: 1999-08-26  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; TYPE: PRT  
; ORGANISM: Gelonium multiflorum  
US-09-645-603B-2

Query Match 100.0%; Score 1287; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.2e-124;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLDTSVSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
Db 1 GLDTSVSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
Db 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
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Db 121 AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
Db 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
Db 241 ALLKFVDKDPK 251

RESULT 12  
US-07-901-707-2  
; Sequence 2, Application US/07901707  
; Patent No. 5376546  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Steve P.  
; APPLICANT: Lane, Julie A.  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; COMPOSITION AND USE FOR RIBOSOME-INACTIVATING PROTEINS

NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/901,707  
; FILING DATE: 19920619  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5376546and, Greta S.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27129/30910  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-5750  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-901-707-2  
Query Match 99.8%; Score 1284; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-124;  
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GLDTSVSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
Db 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
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Db 121 AYRETTDLGIEPLRIGIKKLDENADNPKTEIASLLVVIQWSEAAARFTFIENQIRNN 180  
QY 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
Db 181 FQOIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
Db 241 ALLKFVDKDPK 251

RESULT 13  
US-07-988-430-2  
; Sequence 2, Application US/07988430  
; Patent No. 5416202  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping

;  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Marehall, O'Toole, Gerstein, Murray &  
; ADDRESSES: Bicknell,  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,430  
; FILING DATE: 19921209  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5416202and, Greta E.  
; REGISTRATION NUMBER: 35302  
; REFERENCE/DOCKET NUMBER: 31133  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-988-430-2

Query Match 99.8%; Score 1284; DB 1; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-124;  
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDAIDNYKPTIEASSLLVVIQWSEAAARFTFIEQIRNN 180  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 AYRETTDLGIEPLRIGIKKLDAIDNYKPTIEASSLLVVIQWSEAAARFTFIEQIRNN 180  
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFDKDPK 251  
Db |||||||||||  
241 ALLKFDKDPK 251

RESULT 14

PCT-US92-09487-2

; Sequence 2, Application PC/TUS9209487

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

;  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroli, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSES: Bicknell,  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09487  
; FILING DATE: 19921104  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35302  
; REFERENCE/DOCKET NUMBER: 31133  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US92-09487-2

Query Match 99.8%; Score 1284; DB 4; Length 251;  
Best Local Similarity 99.6%; Pred. No. 2.5e-124;  
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 GLDTSFSTKGATYITYVNFNLRLVKLPKPGNSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDAIDNYKPTIEASSLLVVIQWSEAAARFTFIEQIRNN 180  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 AYRETTDLGIEPLRIGIKKLDAIDNYKPTIEASSLLVVIQWSEAAARFTFIEQIRNN 180  
QY 181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 FOQIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFDKDPK 251  
Db |||||||||||  
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RESULT 15



US-08-621-803-259  
; Sequence 259, Application US/08621803  
; Patent No. 5851802  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/621,803  
; FILING DATE: 22-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 259:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-621-803-259

Query Match 99.8%; Score 1284; DB 1; Length 293;  
Best Local Similarity 99.6%; Pred. No. 3.1e-124; Mismatches 0; Indels 0; Gaps 0;  
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60  
DB 23 GLDTSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 82  
QY 61 QQLABIAIDVTSVYVGVQVRNRSYFFKDDAPDAAYEGLPKNTIKTRLHFGGYSYPSLEGEK 120  
DB 83 QQLABIAIDVTSVYVGVQVRNRSYFFKDDAPDAAYEGLPKNTIKTRLHFGGYSYPSLEGEK 142  
QY 121 AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180  
DB 143 AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 202  
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 203 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 262  
QY 241 ALLKFVDKDPK 251  
DB 263 ALLKFVDKDPK 273

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Job time : 51.0148 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 163.937 Seconds  
(without alignments)  
639.727 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTSFSTKGATYYVNF.....AVDQVKPALKLFVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	251	3	US-09-765-527-247 Sequence 247, App
2	1287	100.0	251	4	US-10-127-890-2 Sequence 2, Appli
3	1287	100.0	251	5	US-10-717-243-2 Sequence 2, Appli
4	1287	100.0	316	4	US-10-074-596-1 Sequence 1, Appli
5	1287	100.0	498	5	US-10-964-195-13 Sequence 13, Appl
6	1287	100.0	507	4	US-10-074-596-11 Sequence 11, Appl
7	1284	99.8	293	3	US-09-765-527-259 Sequence 259, App
8	1284	99.8	309	3	US-09-765-527-253 Sequence 253, App
9	1284	99.8	332	3	US-09-765-527-251 Sequence 251, App
10	1283	99.7	751	6	US-11-084-080-26 Sequence 26, Appl
11	1282	99.6	251	4	US-10-127-890-108 Sequence 108, App
12	1282	99.6	251	5	US-10-717-243-108 Sequence 108, App
13	1279	99.4	251	4	US-10-127-890-103 Sequence 103, App
14	1279	99.4	251	4	US-10-127-890-104 Sequence 104, App
15	1279	99.4	251	4	US-10-127-890-105 Sequence 105, App
16	1279	99.4	251	4	US-10-127-890-106 Sequence 106, App
17	1279	99.4	251	4	US-10-127-890-109 Sequence 109, App
18	1279	99.4	251	5	US-10-717-243-103 Sequence 103, App
19	1279	99.4	251	5	US-10-717-243-104 Sequence 104, App
20	1279	99.4	251	5	US-10-717-243-105 Sequence 105, App
21	1279	99.4	251	5	US-10-717-243-106 Sequence 106, App
22	1279	99.4	251	5	US-10-717-243-109 Sequence 109, App
23	1278	98.3	251	4	US-10-127-890-99 Sequence 99, Appl
24	1278	99.3	251	4	US-10-127-890-100 Sequence 100, App
25	1278	99.3	251	4	US-10-127-890-102 Sequence 102, App
26	1278	99.3	251	4	US-10-127-890-107 Sequence 107, App
27	1278	99.3	251	5	US-10-717-243-99 Sequence 99, Appl

28	1278	99.3	251	5	US-10-717-243-100 Sequence 100, App
29	1278	99.3	251	5	US-10-717-243-102 Sequence 102, App
30	1278	99.3	251	5	US-10-717-243-107 Sequence 107, App
31	1269	98.6	251	4	US-10-127-890-101 Sequence 101, App
32	1269	98.6	251	5	US-10-717-243-101 Sequence 101, App
33	1261	98.0	251	4	US-10-127-890-110 Sequence 110, App
34	1261	98.0	251	5	US-10-717-243-110 Sequence 110, App
35	1252	97.3	251	4	US-10-127-890-111 Sequence 111, App
36	1252	97.3	251	5	US-10-717-243-111 Sequence 111, App
37	1219.5	94.8	513	5	US-10-926-731A-12 Sequence 12, Appl
38	1208	93.9	506	5	US-10-964-195-11 Sequence 11, Appl
39	346	26.9	263	4	US-10-127-890-4 Sequence 4, Appli
40	346	26.9	263	5	US-10-717-243-4 Sequence 4, Appli
41	343	26.7	267	4	US-10-282-935-1 Sequence 1, Appli
42	343	26.7	267	4	US-10-127-890-1 Sequence 1, Appli
43	343	26.7	267	4	US-10-440-796-1 Sequence 1, Appli
44	343	26.7	267	5	US-10-717-243-1 Sequence 1, Appli
45	343	26.7	576	4	US-10-083-336A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-765-527-247

; Sequence 247, Application US/09765527

; Patent No. US20020006638A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/765,527

; FILING DATE: 18-Jan-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/621,803

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 247:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 251 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 247:

US-09-765-527-247

Query Match: 100.0%; Score 1287; DB 3; Length 251;

Best Local Similarity 100.0%; Pred. No. 6.3e-117; Indels 0; Gaps 0;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GLDTSFSTKGATYYVNFLELRLKPKGNHGIPLLRKCKDDPGKCFVLVLSNDN 60

|||||

Db 1 GLDTSVSTKGTATITVYNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 GQLAEIADVTSVVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120  
Db 61 GQLAEIADVTSVVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180  
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
Db 241 ALLKFVDKDPK 251

RESULT 2  
US-10-127-890-2  
; Sequence 2, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins

NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-127-890-2  
Query Match 100.0%; Score 1287; DB 4; Length 251;  
Best Local Similarity 100.0%; Pred. No. 6.3e-117;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLDTSVSTKGTATITVYNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
Db 1 GLDTSVSTKGTATITVYNFLNELRVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
QY 61 GQLAEIADVTSVVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120  
Db 61 GQLAEIADVTSVVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGSGSYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIOMVSEAAARFTFIENQIRNN 180  
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
Db 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
Db 241 ALLKFVDKDPK 251

RESULT 3  
US-10-717-243-2  
; Sequence 2, Application US/10717243  
; Publication No. US20050054835A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins

NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/717,243  
FILING DATE: 18-Nov-2003  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8899  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-717-243-2

Query Match 100.0%; Score 1287; DB 5; Length 251;  
Best Local Similarity 100.0%; Pred. No. 6.3e-117;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATITTYVNFNLKLVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60  
DB 1 GLDTVSFSTKGATITTYVNFNLKLVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 4  
US-10-074-596-1  
Sequence 1, Application US/10074596  
Publication No. US20030176331A1  
GENERAL INFORMATION:  
APPLICANT: ROSENBLUM, MICHAEL G.  
TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF  
FILE REFERENCE: CLFR:007US  
CURRENT APPLICATION NUMBER: US/10/074,596  
CURRENT FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: 60/268,402  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 316  
TYPE: PRT  
ORGANISM: Gelonium multiflorum  
US-10-074-596-1

Query Match 100.0%; Score 1287; DB 4; Length 316;  
Best Local Similarity 100.0%; Pred. No. 8.6e-117;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATITTYVNFNLKLVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60  
DB 47 GLDTVSFSTKGATITTYVNFNLKLVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 106

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 107 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 166

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180

DB 167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 226  
QY 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 227 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 286  
QY 241 ALLKFVDKDPK 251  
DB 287 ALLKFVDKDPK 297

RESULT 5  
US-10-964-195-13  
Sequence 13, Application US/10964195  
Publication No. US20050163774A1  
GENERAL INFORMATION:  
APPLICANT: Rosenblum et al.  
TITLE OF INVENTION: Immunotoxins Directed Against c-erbB-2 (HER-2/Neu)  
FILE REFERENCE: D5425CIP2  
CURRENT APPLICATION NUMBER: US/10/964,195  
CURRENT FILING DATE: 2004-10-13  
PRIOR APPLICATION NUMBER: US/09/320,156  
PRIOR FILING DATE: 1999-05-26  
PRIOR APPLICATION NUMBER: 08/404,499  
PRIOR FILING DATE: 1995-03-17  
NUMBER OF SEQ ID NOS: 14  
SEQ ID NO 13  
LENGTH: 498  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Polypeptide encoded by the scFv23-gelonin immunotoxin  
US-10-964-195-13

Query Match 100.0%; Score 1287; DB 5; Length 498;  
Best Local Similarity 100.0%; Pred. No. 1.6e-116;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATITTYVNFNLKLVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 60  
DB 247 GLDTVSFSTKGATITTYVNFNLKLVKLPKGNHGIPLLRKCCDDPKCFVLVSLNDN 306

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 307 GQLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 366

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 180  
DB 367 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASSLLVVIQMVSEAAARFTFIENQIRNN 426

QY 181 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
DB 427 FQORIRPANNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTAVDQVKPKI 486

QY 241 ALLKFVDKDPK 251  
DB 487 ALLKFVDKDPK 497

RESULT 6  
US-10-074-596-11  
Sequence 11, Application US/10074596  
Publication No. US20030176331A1  
GENERAL INFORMATION:  
APPLICANT: ROSENBLUM, MICHAEL G.  
TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF  
FILE REFERENCE: CLFR:007US  
CURRENT APPLICATION NUMBER: US/10/074,596  
CURRENT FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: 60/268,402



SEQUENCE DESCRIPTION: SEQ ID NO: 253;  
US-09-765-527-253

Query Match 99.8%; Score 1284; DB 3; Length 309;  
Best Local Similarity 99.6%; Pred. No. 1.6e-116;  
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
Db GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 82  
  
Qy 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
Db GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 142  
  
Qy 121 AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQWSEARFTFIENQIRNN 180  
Db AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQWSEARFTFIENQIRNN 202  
  
Qy 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262  
  
Qy 241 ALLKFPVDKDPK 251  
Db ALLKFPVDKDPK 273

## RESULT 9

US-09-765-527-251  
; Sequence 251, Application US/09765527  
; Patent No. US20020006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 251:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 251:  
US-09-765-527-251

Query Match 99.8%; Score 1284; DB 3; Length 332;

Best Local Similarity 99.6%; Pred. No. 1.8e-116;  
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
Db GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 82  
  
Qy 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
Db GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 142  
  
Qy 121 AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQWSEARFTFIENQIRNN 180  
Db AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQWSEARFTFIENQIRNN 202  
  
Qy 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 262  
  
Qy 241 ALLKFPVDKDPK 251  
Db ALLKFPVDKDPK 273

## RESULT 10

US-11-084-080-26  
; Sequence 26, Application US/11084080  
; Publication No. US20050238642A1  
; GENERAL INFORMATION:  
; APPLICANT: BAKER, Matthew  
; APPLICANT: CARR, Francis J.  
; APPLICANT: HELLEDOORN, Koen  
; APPLICANT: CIZEAU, Jeannick  
; APPLICANT: MACDONALD, Glen Christopher  
; APPLICANT: ENTWISTLE, Joycelyn  
; APPLICANT: BOSCH, Denis Georges  
; APPLICANT: GLOVER, Nicholas Ronald  
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND USES  
; FILE REFERENCE: 10241-44  
; CURRENT APPLICATION NUMBER: US/11/084,080  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US 60/554,580  
; PRIOR FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: US 60/630,571  
; PRIOR FILING DATE: 2004-11-26  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 26  
; LENGTH: 751  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VB6-845-gelonin  
US-11-084-080-26

Query Match 99.7%; Score 1283; DB 6; Length 751;  
Best Local Similarity 99.6%; Pred. No. 7e-116;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 60  
Db GLDTSFSTKGATYITVNFNLRLVKLPKGNHSHGIPLLRKKDDPGKCFVLVALSNDN 313  
  
Qy 61 GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
Db GOLAEIADVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGYSYPSLEGEK 373  
  
Qy 121 AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQWSEARFTFIENQIRNN 180  
Db AYRETTDLGIEPLRIGIKLDENADNYKPTETIASLLVVIQWSEARFTFIENQIRNN 433  
  
Qy 181 FQOIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

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Db      434  FQOIRPNTNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 493
Qy      241  ALLKFVDKDPK 251
Db      494  ALLKFVDKDPK 504

RESULT 11
US-10-127-890-108
; Sequence 108, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108
Query Match          99.6%; Score 1282; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.9e-116; Indels 0; Gaps 0;
Matches 250; Conservative 0; Mismatches 1;

Qy      1  GLDTSFSTKGATYYTYVNFNLRLVGLKPEGNHSHGIPLLRKKCDGPKCFVLVSLNDN 60
Db      1  GLDTSFSTKGATYYTYVNFNLRLVGLKPEGNHSHGIPLLRKKCDGPKCFVLVSLNDN 60

Qy      61  GOLAEIADVTSVVVGQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
Db      61  GOLAEIADVTSVVVGQVNRNSYFFKADAPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120
Qy      121  AYRETTDLGIEPLRIGIKLDENADINYKPTIEIASSLLVVIQMVSEAAARFTFIENQIRNN 180
Db      121  AYRETTDLGIEPLRIGIKLDENADINYKPTIEIASSLLVVIQMVSEAAARFTFIENQIRNN 180
Qy      181  FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db      181  FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Qy      241  ALLKFVDKDPK 251
Db      241  ALLKFVDKDPK 251

RESULT 12
US-10-717-243-108
; Sequence 108, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-717-243-108
```



Query Match 99.6%; Score 1282; DB 5; Length 251;  
Best Local Similarity 99.6%; Pred. No. 1.9e-116;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKGNHSHGIPLLRKKDDPKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKGNHSHGIPLLRKKDDPKCFVLVALSNDN 60  
QY 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFPKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120  
DB 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFPKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVWIQMVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVWIQMVSEAAARFTFIENQIRNN 180  
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 13  
US-10-127-890-103  
; Sequence 103, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins

NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155

TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 103:  
US-10-127-890-103

Query Match 99.4%; Score 1279; DB 4; Length 251;  
Best Local Similarity 99.6%; Pred. No. 3.8e-116;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKGNHSHGIPLLRKKDDPKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYVFNFLNLRVVKLPKGNHSHGIPLLRKKDDPKCFVLVALSNDN 60  
QY 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFPKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120  
DB 61 GOLAEIAIDVTSVYVVGQVNRNRSYFFPKADPDAAYEGLFKNTIKTRLHFGSGYSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVWIQMVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIEASSLLVWIQMVSEAAARFTFIENQIRNN 180  
QY 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FOORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 14  
US-10-127-890-104  
; Sequence 104, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

```
/
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 104:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-127-890-104

Query Match          99.4%; Score 1279; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLNRVCLKPESGSHGIPLLRKKCDPDKCFVLVSLNDN 60
DB 1 GLDVSFSTKGATITTYVNFNLNRVCLKPESGSHGIPLLRKKCDPDKCFVLVSLNDN 60

QY 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 15
US-10-127-890-105
/ Sequence 105, Application US/10127890
/ Publication No. US20030166196A1
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ NUMBER OF SEQUENCES: 173
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/127,890
/ FILING DATE: 23-Apr-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/646,360
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/
/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 105:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 251 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-127-890-105

Query Match          99.4%; Score 1279; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.8e-116;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLNRVCLKPESGSHGIPLLRKKCDPDKCFVLVSLNDN 60
DB 1 GLDVSFSTKGATITTYVNFNLNRVCLKPESGSHGIPLLRKKCDPDKCFVLVSLNDN 60

QY 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

Search completed: February 10, 2006, 10:44:45
Job time : 164.937 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 136.614 Seconds  
(without alignments)  
807.265 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDTVSFTKGTATYYTNF.....AVDQVKPKIALKFVDKPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq 21:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	251	2	AAR63903 Type I ri
2	1287	100.0	251	8	ADG63044 Gelonium
3	1287	100.0	316	5	ABG71551 G. multif
4	1287	100.0	498	9	AEB68722 scFv23-ge
5	1287	100.0	507	5	ABG71552 Murine sc
6	1284	99.8	293	2	Aaw29300 BPI pepti
7	1284	99.8	309	2	Aaw29303 BPI pepti
8	1284	99.8	332	2	Aaw29294 BPI pepti
9	1282	98.6	251	2	AAR63923 Type I RI
10	1279	99.4	251	2	AAR63921 Type I RI
11	1279	99.4	251	2	AAR63918 Type I RI
12	1279	99.4	251	2	AAR63920 Type I RI
13	1279	99.4	251	2	AAR63919 Type I RI
14	1279	99.4	251	2	AAR63924 Type I RI
15	1278	99.3	251	2	AAR63922 Type I RI
16	1278	99.3	251	2	AAR63917 Type I RI
17	1278	99.3	251	2	AAR63912 Type I RI
18	1275	99.1	251	2	AAR74177 Type I ri
19	1269	98.6	251	2	AAR37291 Plant typ
20	1269	98.6	251	2	AAR63914 Type I RI
21	1261	98.0	251	2	AAR63915 Type I RI
22	1252	97.3	251	2	AAR63916 Type I RI
23	1242.5	96.5	258	2	AAR22227 Gelonin t
24	1208	93.9	506	9	AEB68720 scFv23-ge

25	1176	91.4	235	2	AAR63913	AAR63913 Type I RI
26	346	26.9	263	2	AAR63905	AAR63905 Type I ri
27	346	26.9	263	2	AAR74179	AAR74179 Type I ri
28	346	26.9	263	8	ADG63043	ADG63043 Momordica
29	344	26.7	565	1	AAP50166	Sequence
30	344	26.7	565	4	AAG78300	Castor be
31	344	26.7	574	1	AAP70325	Sequence
32	343	26.7	267	2	AAR30722	AAR30722 Ricin A c
33	343	26.7	267	2	AAR37290	Ricin A c
34	343	26.7	267	2	AAR63902	Ricin A-c
35	343	26.7	267	3	AB119265	Amino aci
36	343	26.7	267	7	ADC24288	Ricin tox
37	343	26.7	268	2	AAR39570	Sequence
38	343	26.7	290	2	AAR21699	AAR21699 Ricin A-c
39	343	26.7	290	2	AAW25136	Ricin A-c
40	343	26.7	332	1	AAP70097	Ricin A-
41	343	26.7	332	1	AAP70838	Sequence
42	343	26.7	332	1	AAP95639	Ricin A e
43	343	26.7	554	2	AAR70827	Anti-cata
44	343	26.7	562	1	AAP90079	Ricin D.
45	343	26.7	565	4	AAG78304	Modified

## ALIGNMENTS

RESULT 1

AAR63903

ID AAR63903 standard; protein; 251 AA.

AC AAR63903;

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Type I ribosome-inactivating protein gelonin.

XX Type I ribosome-inactivating proteins; RIPs; gelonin;  
KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
KW graft-versus-host disease.

OS Gelonium multiflorum.

XX WO9426910-A1.

XX PD 24-NOV-1994.

XX PF 12-MAY-1994; 94WO-US005348.

XX PR 12-MAY-1993; 93US-00064691.

XX PA (XOMA ) XOMA CORP.

XX PI Better MD, Carroll SF, Studnicka GW;

XX DR WPI; 1995-006804/01.

XX DR N-PSDB; AAQ75532.

XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
are suitable for use as components of cytotoxic therapeutic agents.  
Example 1; Fig 1; 221pp; English.

XX CC AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)  
gelonin, one of the nine RIPs described in AAR63903-Re3911. RIPs are key  
components of cytotoxic therapeutic agents (CTAs), which include gene  
fusion products and immunoconjugates. CTAs may be used to selectively  
eliminate any cell type to which a RIP component is targeted, by the  
specific binding capacity of the second component of the agent. They can  
be used in the treatment of diseases where the elimination of a  
particular cell type is desired, such as autoimmune disease, cancer and  
graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

SQL Sequence 251 AA;  
Query Match 100.0%; Score 1287; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.8e-125;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60  
QY 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120  
DB 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180  
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 2  
ADG63044  
ID ADG63044 standard; protein; 251 AA.  
XX AC ADG63044;  
XX DT 11-MAR-2004 (first entry)  
XX DE Gelonium anti-HIV protein 31kDa (GAP31).  
XX KW anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;  
KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.  
XX OS Gelonium multiflorum.  
XX US6652861-B1.  
XX PN 25-NOV-2003.  
XX PD 25-AUG-2000; 2000US-00645603.  
XX PF 26-AUG-1999; 99US-0150885P.  
XX PR (UYN) UNIV NEW YORK STATE.  
XX PA Lee-Huang S;  
XX PI WPI; 2004-050519/05.  
XX DR New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and  
PT antiviral activity, useful for treating human immunodeficiency virus  
PT infection or tumor.  
XX PS Example 1; SEQ ID NO 2; 22pp; English.  
XX CC The invention describes an isolated peptide or polypeptide having an anti-  
CC -tumour and antiviral activity. Also described is a composition  
CC comprising the isolated peptide or polypeptide, and a carrier, excipient  
CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or  
CC polypeptides. The peptide or polypeptide is useful for treating HIV  
CC infection, and tumour. This is the amino acid sequence of Gelonium anti-  
CC HIV protein 30kDa (MAP30).  
XX SQ Sequence 251 AA;  
Query Match 100.0%; Score 1287; DB 8; Length 251;

Best Local Similarity 100.0%; Pred. No. 1.8e-125;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60  
DB 1 GLDVSFSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKKCDPDKCFVLVALSNDN 60  
QY 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120  
DB 61 QGLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLEGEK 120  
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTBIASSLLVVIQWSEAAARFTFIENQIRNN 180  
QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251  
RESULT 3  
ABG71551  
ID ABG71551 standard; protein; 316 AA.  
XX AC ABG71551;  
XX DT 08-JAN-2003 (first entry)  
XX DE G. multiflorum recombinant gelonin (rGel) toxin.  
XX KW Modified protein; reduced antigenicity; modified toxin; gelonin;  
KW designer toxin; immunotoxin; proteinaceous compound; cancer;  
KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;  
KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;  
KW inflammatory disease; cardiovascular disease; diabetes;  
KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;  
KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;  
KW recombinant gelonin; rGel.  
XX OS Gelonium multiflorum.  
XX PN WO200269886-A2.  
XX PD 12-SEP-2002.  
XX PF 12-FEB-2002; 2002WO-US004195.  
XX PR 12-FEB-2001; 2001US-0268402P.  
XX PA (RERE-) RES DEV FOUND.  
XX PI Rosenblum MG, Cheung L;  
XX DR WPI; 2002-750431/81.  
XX DR N-PSDB; ABS556021.  
XX PT Generating a modified protein with reduced antigenicity for treating  
PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region  
PT antigenic in the first subject using antiserum from either the first or a  
PT second subject.  
XX PS Claim 63; Page 169-170; 176pp; English.  
XX CC The present invention relates to a method of generating a modified  
CC protein with reduced antigenicity while maintaining its biological  
CC activity. The method comprises identifying a region of the protein that  
CC is antigenic in a first subject using antiserum from either the first  
CC subject or a second subject of the same species as the first subject. In  
CC particular the invention discloses modified toxin compounds, for example

CC gelonin toxin derived from Gelonium multiflorum, that are truncated  
 CC and/or possess reduced antigenicity. Such designer toxins have  
 CC therapeutic, diagnostic, and preventative benefits, particularly as  
 CC immunotoxins. The method of the invention is useful for generating  
 CC proteinaceous compounds with less antigenicity. The immunotoxin and  
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,  
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,  
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall  
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The  
 CC compositions of the invention are also useful for treating microbial  
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune  
 CC diseases, hyperproliferative disorders including cancer, leukemias,  
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic  
 CC diseases, and diabetes. The method provides less antigenic proteins,  
 CC peptides and polypeptides, which are more effective than prior art. The  
 CC present sequence represents G. multiflorum recombinant gelonin (rGel)  
 XX  
 XX Sequence 316 AA;

Query Match 100.0%; Score 1287; DB 5; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-125;  
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60  
 DB 47 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 106

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 120  
 DB 107 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 166

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQWSEAAARFTFIEQIRNN 180  
 DB 167 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQWSEAAARFTFIEQIRNN 226

QY 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEBRANGKYYVTAVDQVKPKI 240  
 DB 227 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEBRANGKYYVTAVDQVKPKI 286

QY 241 ALLKPFVDKDPK 251  
 DB 287 ALLKPFVDKDPK 297

RESULT 4  
 ID AEB68722 standard; protein; 498 AA.

AC AEB68722;

DT 06-OCT-2005 (first entry)

DE scFv23-gelonin immunotoxin amino acid sequence SEQ ID NO:13.

XX antibody engineering; c-erbB-2 protein; toxin; gelonin; cytostatic;  
 KW immunotoxin; neoplasm.

XX Synthetic.

XX US2005163774-A1.

XX 28-JUL-2005.

XX 13-OCT-2004; 2004US-00964195.

XX 10-APR-1992; 92US-00867728.

XX 09-DEC-1993; 93US-00164638.

XX 02-SEP-1994; 94US-00300082.

XX 17-MAR-1995; 95US-00404499.

XX 26-MAY-1999; 99US-00320156.

XX (RERE-) RES DEV FOUND.

XX PA

PI Rosenblum M, Shawver LK;  
 XX WPI; 2005-561813/57.  
 DR N-PSDB; AEB68721.  
 XX  
 PT New immunotoxins directed against c-erbB-2 related surface antigens,  
 PT useful for treating neoplastic diseases, e.g. carcinoma or  
 PT adenocarcinoma.  
 XX  
 PS Disclosure; SEQ ID NO 13; 60pp; English.  
 XX  
 CC The invention relates to a composition comprising a conjugate of an  
 CC antibody exhibiting binding specificity for an extracellular epitope of c  
 CC -erbB-2 protein and a plant derived toxin, where the toxin is  
 CC pharmacologically effective against neoplastic cells and is selected from  
 CC gelonin, full length recombinant gelonin, functional gelonin fragments or  
 CC functional gelonin derivatives. Also described is a pharmaceutical  
 CC composition comprising the composition above and a pharmaceutical  
 CC vehicle. For treating neoplastic diseases, e.g. human mammary carcinomas,  
 CC human ovarian carcinomas, lung carcinomas, gastric tumors, salivary gland  
 CC adenocarcinomas, or colon adenocarcinomas. The present sequence  
 CC represents a scFv23-gelonin amino acid sequence, which is used in an  
 CC example from the present invention.

XX Sequence 498 AA;

Query Match 100.0%; Score 1287; DB 9; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-125;  
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60  
 DB 247 GLDVSFSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 306

QY 61 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 120  
 DB 307 GQLAEIAIDVTSVYVGVQVRNRSYFFKADPAAYEGLPKNTIKTRLHFGSGSYPSLEGK 366

QY 121 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQWSEAAARFTFIEQIRNN 180  
 DB 367 AYRETTDLGIEPLRIGIKKLDENADNYKPTIASLLVVIQWSEAAARFTFIEQIRNN 426

QY 181 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEBRANGKYYVTAVDQVKPKI 240  
 DB 427 FQQRIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEBRANGKYYVTAVDQVKPKI 486

QY 241 ALLKPFVDKDPK 251  
 DB 487 ALLKPFVDKDPK 497

RESULT 5

ABG71552

ID ABG71552 standard; protein; 507 AA.

XX AC ABG71552;

XX 08-JAN-2003 (first entry)

XX Murine scfMEL/G. multiflorum rGel fusion protein.

XX Modified protein; reduced antigenicity; modified toxin; gelonin;  
 KW designer toxin; immunotoxin; proteinaceous compound; cancer;  
 KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;  
 KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;  
 KW inflammatory disease; cardiovascular disease; diabetes;  
 KW pathogenic disease; cytostatic; antitumor; antifungal;  
 KW antigen; antidiabetic; virucide; protozoacide; fungicide; antibacterial;  
 KW murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;  
 KW scfMEL/rGel; mutant; mutein.

XX Mus sp.

OS Gelonium multiflorum.

OS Synthetic.  
 OS Chimeric.  
 XX WO200269886-A2.  
 PD 12-SEP-2002.  
 XX  
 XX 12-FEB-2002; 2002WO-US0041195.  
 XX  
 XX 12-FEB-2001; 2001US-0268402P.  
 XX  
 XX (RERE-) RES DEV FOUND.  
 XX  
 XX Rosenblum MG, Cheung L;  
 XX  
 XX WPI; 2002-750431/81.  
 XX N-PSDB; ABS56029.  
 XX  
 XX Generating a modified protein with reduced antigenicity for treating  
 XX cancer, AIDS, autoimmune diseases, comprises identifying a protein region  
 XX antigenic in the first subject using antiserum from either the first or a  
 XX second subject.  
 XX  
 XX Disclosure; Page 174-176; 176pp; English.  
 XX  
 XX The present invention relates to a method of generating a modified  
 XX protein with reduced antigenicity while maintaining its biological  
 XX activity. The method comprises identifying a region of the protein that  
 XX is antigenic in a first subject using antiserum from either the first  
 XX subject or a second subject of the same species as the first subject. In  
 XX particular the invention discloses modified toxin compounds, for example  
 XX gelonin toxin derived from Gelonium multiflorum, that are truncated  
 XX and/or possess reduced antigenicity. Such designer toxins have  
 XX therapeutic, diagnostic, and preventative benefits, particularly as  
 XX immunotoxins. The method of the invention is useful for generating  
 XX proteinaceous compounds with less antigenicity. The immunotoxin and  
 XX gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,  
 XX skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,  
 XX bone, bone marrow, head and neck, cervical, oesophagus, eye, gall  
 XX bladder, kidney, adrenal glands, heart, colon, or blood cancer. The  
 XX compositions of the invention are also useful for treating microbial  
 XX pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmunity  
 XX diseases, hyperproliferative disorders including cancer, leukaemias,  
 XX arthritis, inflammatory diseases, cardiovascular diseases, pathogenic  
 XX diseases, and diabetes. The method provides less antigenic proteins,  
 XX peptides and polypeptides, which are more effective than prior art. The  
 XX present sequence represents murine single-chain ZMB-018 antibody/G.  
 XX multiflorum recombinant gelonin (rGel) (scfvMEL/rGel) fusion protein  
 XX  
 XX Sequence 507 AA;  
 XX  
 XX Query Match 100.0%; Score 1287; DB 5; Length 507;  
 XX Best Local Similarity 100.0%; Pred. No. 5, 1e-125;  
 XX Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPKGNHIGIPLLRKCCDDPGKCFVLVSLNDN 60  
 DB 257 GLDTSFSTKGATITTYVNFNLRLVKLPKGNHIGIPLLRKCCDDPGKCFVLVSLNDN 316  
 QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAEGLFKNTIKTRLHFGGSSYPSLEGK 120  
 DB 317 GQLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAEGLFKNTIKTRLHFGGSSYPSLEGK 376  
 QY 121 AVRETTDLGIEPLRIGIKKL DENAIDNYKPTETASLLVVIQWSEAAFTFIENQIRNN 180  
 DB 377 AVRETTDLGIEPLRIGIKKL DENAIDNYKPTETASLLVVIQWSEAAFTFIENQIRNN 436  
 QY 181 FQQRIRPANNTISLENKWKLSFQIRTS GANGFSEAVELERANGKYYVTVADQVKPKI 240  
 DB 437 FQQRIRPANNTISLENKWKLSFQIRTS GANGFSEAVELERANGKYYVTVADQVKPKI 496  
 QY 241 ALLKFFVDKDPK 251  
 |||||

Db 497 ALLKFFVDKDPK 507  
 RESULT 6  
 AAW29300  
 ID AAW29300 standard; protein; 293 AA.  
 XX  
 AC AAW29300;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 DE BPI peptide fusion protein PING3797 vector construct protein.  
 XX  
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;  
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;  
 KW fungicidal; recombinant DNA; vector.  
 XX  
 OS Synthetic.  
 OS Pectobacterium carotovorum.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 PN WO9735009-A1.  
 XX  
 PD 25-SEP-1997.  
 XX  
 PF 18-MAR-1997; 97WO-US005287.  
 XX  
 PR 22-MAR-1996; 96US-00621803.  
 XX  
 PA (XOMA ) XOMA CORP.  
 XX  
 PI Better MD;  
 XX  
 DR WPI; 1997-480215/44.  
 DR N-PSDB; AAT86336.  
 XX  
 XX Recombinant production of bactericidal/permeability increasing protein -  
 XX by expression as a fusion protein in microbial host cells, then cleaving  
 XX the BPI peptide from the carrier.  
 XX  
 XX Example 1; Page 160-161; 186pp; English.  
 XX  
 XX A new recombinant DNA vector construct has been developed which encodes a  
 XX fusion protein and is suitable for introduction into a bacterial host.  
 XX The vector comprises: (a) DNA encoding at least one cationic  
 XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a  
 XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site  
 XX located between (a) and (b). The present sequence represents the protein  
 XX from the PING3797 vector construct which codes for a BPI fusion protein.  
 XX The peptides have many uses including the treatment of bacterial and  
 XX fungal infections. BPI peptides also bind to endotoxins and heparin,  
 XX neutralising their effects. The peptides have further been shown to  
 XX inhibit angiogenesis (partly due to heparin-binding activity). The fusion  
 XX proteins have been found to be expressed in large amounts without  
 XX significant proteolysis, and in some cases are actually secreted from the  
 XX host cells. This allows the indirect production of anti-microbial BPI  
 XX peptides in microbial hosts  
 XX  
 XX Sequence 293 AA;  
 XX  
 XX Query Match 99.8%; Score 1284; DB 2; Length 293;  
 XX Best Local Similarity 99.6%; Pred. No. 4, 7e-125;  
 XX Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLDTSFSTKGATITTYVNFNLRLVKLPKGNHIGIPLLRKCCDDPGKCFVLVSLNDN 60  
 DB 23 GLDTSFSTKGATITTYVNFNLRLVKLPKGNHIGIPLLRKCCDDPGKCFVLVSLNDN 82  
 QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAEGLFKNTIKTRLHFGGSSYPSLEGK 120  
 DB 83 GQLAEIAIDVTSVYVVGQVNRNSYFFKDAADAAEGLFKNTIKTRLHFGGSSYPSLEGK 142

QY 121 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180  
 DB 143 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 202  
 QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCYVTVAVDQVKPKI 240  
 DB 203 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCYVTVAVDQVKPKI 262  
 QY 241 ALLKPFVDKDPK 251  
 DB 263 ALLKPFVDKDPK 273

RESULT 7  
 AAW29303  
 ID AAW29303 standard; protein; 309 AA.  
 XX  
 AC AAW29303;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 DE BPI peptide fusion protein PING3795 vector construct protein.  
 XX  
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;  
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;  
 KW fungicidal; recombinant DNA; vector.  
 XX  
 OS Synthetic.  
 OS Pectobacterium carotovorum.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 PN WO9735009-A1.  
 XX  
 PD 25-SEP-1997.  
 XX  
 PF 18-MAR-1997; 97WO-US005287.  
 XX  
 PR 22-MAR-1996; 96US-00621803.  
 XX  
 PA (XOMA ) XOMA CORP.  
 XX  
 PI Better MD;  
 XX  
 WPI; 1997-480215/44.  
 DR N-PSDB; AAT86341.  
 XX  
 PT Recombinant production of bactericidal/permeability increasing protein -  
 PT by expression as a fusion protein in microbial host cells, then cleaving  
 PT the BPI peptide from the carrier.  
 XX  
 PS Example 1; Page 152-153; 186pp; English.  
 XX  
 CC A new recombinant DNA vector construct has been developed which encodes a  
 CC fusion protein and is suitable for introduction into a bacterial host.  
 CC The vector comprises: (a) DNA encoding at least one cationic  
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a  
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site  
 CC located between (a) and (b). The present sequence represents the protein  
 CC from the PING3795 vector construct which codes for a BPI fusion protein.  
 CC The peptides have many uses including the treatment of bacterial and  
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,  
 CC neutralising their effects. The peptides have further been shown to  
 CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion  
 CC proteins have been found to be expressed in large amounts without  
 CC significant proteolysis, and in some cases are actually secreted from the  
 CC host cells. This allows the indirect production of anti-microbial BPI  
 CC peptides in microbial hosts  
 XX  
 SQ Sequence 309 AA;

Query Match 99.8%; Score 1284; DB 2; Length 309;  
 Best Local Similarity 99.6%; Pred. No. 5.1e-125;

Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLDTSVSTKGTATITTYVNFNLRLRVKLPKPSGSHGIPLLRKKCDPDKCFVLVALSNDN 60  
 DB 23 GLDTSVSTKGTATITTYVNFNLRLRVKLPKPSGSHGIPLLRKKCDPDKCFVLVALSNDN 82  
 QY 61 GOLABIAIDVTSVTVGVQVNRNSYFFPKADAPDAAYEGLFKQNTIKTRLHFGSGYPSLEGEK 120  
 DB 83 GOLABIAIDVTSVTVGVQVNRNSYFFPKADAPDAAYEGLFKQNTIKTRLHFGSGYPSLEGEK 142  
 QY 121 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 180  
 DB 143 AYRETTDLGIEPLRIGIKKLDNAIDNYKPTBIASSLLVVIQMVSEAAARFTFIENQIRNN 202  
 QY 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCYVTVAVDQVKPKI 240  
 DB 203 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKCYVTVAVDQVKPKI 262  
 QY 241 ALLKPFVDKDPK 251  
 DB 263 ALLKPFVDKDPK 273

RESULT 8  
 AAW29294  
 ID AAW29294 standard; protein; 332 AA.  
 XX  
 AC AAW29294;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 DE BPI peptide fusion protein PING3793 vector construct protein.  
 XX  
 KW Bactericidal/permeability increasing peptide; BPI; fusion protein;  
 KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;  
 KW fungicidal; recombinant DNA; vector.  
 XX  
 OS Synthetic.  
 OS Pectobacterium carotovorum.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 PN WO9735009-A1.  
 XX  
 PD 25-SEP-1997.  
 XX  
 PF 18-MAR-1997; 97WO-US005287.  
 XX  
 PR 22-MAR-1996; 96US-00621803.  
 XX  
 PA (XOMA ) XOMA CORP.  
 XX  
 PI Better MD;  
 XX  
 WPI; 1997-480215/44.  
 DR N-PSDB; AAT86332.  
 XX  
 PT Recombinant production of bactericidal/permeability increasing protein -  
 PT by expression as a fusion protein in microbial host cells, then cleaving  
 PT the BPI peptide from the carrier.  
 XX  
 PS Example 1; Page 148-150; 186pp; English.  
 XX  
 CC A new recombinant DNA vector construct has been developed which encodes a  
 CC fusion protein and is suitable for introduction into a bacterial host.  
 CC The vector comprises: (a) DNA encoding at least one cationic  
 CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a  
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site  
 CC located between (a) and (b). The present sequence represents the protein  
 CC from the PING3793 vector construct which codes for a BPI fusion protein.  
 CC The peptides have many uses including the treatment of bacterial and  
 CC fungal infections. BPI peptides also bind to endotoxins and heparin,  
 CC neutralising their effects. The peptides have further been shown to

CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion  
 CC proteins have been found to be expressed in large amounts without  
 CC significant proteolysis, and in some cases are actually secreted from the  
 CC host cells. This allows the indirect production of anti-microbial BPI  
 CC peptides in microbial hosts  
 XX  
 SQ Sequence 332 AA;

Query Match 99.8%; Score 1284; DB 2; Length 332;  
 Best Local Similarity 99.6%; Pred. No. 5.6e-125;  
 Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLDVSFSTKGATYYVNFLELRVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60  
 DB 23 GLDVSFSTKGATYYVNFLELRVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 82  
 QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 DB 83 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 142  
 QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180  
 DB 143 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 202  
 QY 181 FOORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKKYVYTTAVDQVKPKI 240  
 DB 203 FOORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKKYVYTTAVDQVKPKI 262  
 QY 241 ALLKFVDKDPK 251  
 DB 263 ALLKFVDKDPK 273

RESULT 9  
 AAR63923  
 ID AAR63923 standard; protein; 251 AA.  
 XX  
 AC AAR63923;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 XX Type I RIP gelonin analog Gel(C103).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPS; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PP 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 PI Better MD, Carroll SF, Studnicka GM;  
 XX  
 XX WPI; 1995-006804/01.  
 XX  
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 XX Example 3; Page 187-188; 221pp; English.  
 PS  
 XX  
 XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.  
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to

CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 251 AA;

Query Match 99.6%; Score 1282; DB 2; Length 251;  
 Best Local Similarity 99.6%; Pred. No. 6.1e-125;  
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GLDVSFSTKGATYYVNFLELRVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60  
 DB 1 GLDVSFSTKGATYYVNFLELRVKLPKGNHSHGIPLLRKKCDPDKCFVLVALSNDN 60  
 QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENADINYKPTETIASLLVVIQWSEAAARFTFIENQIRNN 180  
 QY 181 FOORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKKYVYTTAVDQVKPKI 240  
 DB 181 FOORIRPANNTISLENKWGKLSFQIRTSANGMFSEAVELERANGKKYVYTTAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 10  
 AAR63921  
 ID AAR63921 standard; protein; 251 AA.  
 XX  
 AC AAR63921;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 XX Type I RIP gelonin analog Gel(C10).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPS; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PP 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 PI Better MD, Carroll SF, Studnicka GM;  
 XX  
 XX WPI; 1995-006804/01.  
 XX  
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 XX Example 3; Page 186; 221pp; English.  
 PS  
 XX  
 XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPS described in AAR63903-R63911.  
 CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to



CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;  
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60  
 DB 1 GLDVSFSTCGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60  
 QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAADAAVEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
 DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAADAAVEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAARPTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAARPTFIENQIRNN 180  
 QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 11  
 AAR63918  
 ID AAR63918 standard; protein; 251 AA.  
 XX  
 AC AAR63918;  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 DE Type I RIP gelonin analog Gel (C248).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 PI Better MD, Carroll SF, Studnicka GM;  
 XX  
 DR WPI; 1995-006804/01.  
 XX  
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 XX Example 3; Page 183-184; 221pp; English.  
 XX  
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.

CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;  
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60  
 DB 1 GLDVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKCDPDKGCFVLVALSNDN 60  
 QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAADAAVEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
 DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPAADAAVEGLFKNTIKTRLHFGGYSYPSLEGEK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAARPTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASSLLVVIQMVSEAAARPTFIENQIRNN 180  
 QY 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 DB 181 FOORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 12  
 AAR63920  
 ID AAR63920 standard; protein; 251 AA.  
 XX  
 AC AAR63920;  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 DE Type I RIP gelonin analog Gel (C244).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 PI Better MD, Carroll SF, Studnicka GM;  
 XX  
 DR WPI; 1995-006804/01.  
 XX  
 PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 XX Example 3; Page 185; 221pp; English.  
 XX  
 CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating

CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX correct PN field.)  
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;  
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GLDTSFSTKGATITTYVNFNLNLRVCLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60  
 DB 1 GLDTSFSTKGATITTYVNFNLNLRVCLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60  
 QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120  
 DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180  
 QY 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 DB 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLCFVDKDPK 251

RESULT 13  
 AAR63919  
 ID AAR63919 standard; protein; 251 AA.  
 XX AAR63919;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 DE Type I RIP gelonin analog Gel(C239).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 PA (XOMA ) XOMA CORP.  
 XX  
 PI Better MD, Carroll SF, Studnicka GM;  
 XX  
 DR WPI; 1995-006804/01.  
 XX  
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 PS Example 3; Page 184; 221pp; English.

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX correct PN field.)  
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1279; DB 2; Length 251;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-124;  
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GLDTSFSTKGATITTYVNFNLNLRVCLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60  
 DB 1 GLDTSFSTKGATITTYVNFNLNLRVCLKPEGNHGIPLLRKKDDPGKCFVLVALSNDN 60  
 QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120  
 DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFKDPADAAVEGLFKNTIKTRLHFGGSYPSLEGK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIEASLLVVIQWSEAAARFTFIENQIRNN 180  
 QY 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 DB 181 FOQIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 14  
 AAR63924  
 ID AAR63924 standard; protein; 251 AA.  
 XX AAR63924;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 DE Type I RIP gelonin analog Gel(C184).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 PA (XOMA ) XOMA CORP.  
 XX  
 PI Better MD, Carroll SF, Studnicka GM;  
 XX  
 DR WPI; 1995-006804/01.  
 XX  
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 PS Example 3; Page 188-189; 221pp; English.

```

XX CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX CC
SQ Sequence 251 AA;

Query Match          99.4%; Score 1279; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.2e-124;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60
DB 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKPFVDKDPK 251
DB 241 ALLKPFVDKDPK 251

```

## RESULT 15

AAR63922 ID AAR63922 standard; protein; 251 AA.

XX AC AAR63922;

XX DT 25-MAR-2003 (revised)

XX DT 27-JUL-1995 (first entry)

XX DE Type I RIP gelonin analog Gel(C60).

XX KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.

XX OS Gelonium multiflorum.

XX PN WO9426910-A1.

XX PD 24-NOV-1994.

XX PF 12-MAY-1994; 94WO-US005348.

XX PR 12-MAY-1993; 93US-00064691.

XX PA (XOMA ) XOMA CORP.

XX PI Better MD, Carroll SF, Studnicka GM;

XX DR WPI; 1995-006804/01.

XX FT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.

XX

PS Example 3; Page 187; 221pp; English.

XX CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX CC

SQ Sequence 251 AA;

Query Match 99.3%; Score 1278; DB 2; Length 251;

Best Local Similarity 99.6%; Pred. No. 1.6e-124;

Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60

DB 1 GLDTSVSTKGATITTYVNFNLRLVKLPKPGNSHGIPLLRKCDPDKGKCFVLVALSNDN 60

QY 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

DB 61 GOLAEIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

DB 121 AYRETTDLGIEPLRIGIKKLDENAIQNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKPFVDKDPK 251

DB 241 ALLKPFVDKDPK 251

Search completed: February 10, 2006, 10:04:59

Job time : 138.614 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:05:19 ; Search time 34.2694 Seconds  
(without alignments)  
704.723 Million cell updates/sec

Title: US-10-717-243-2  
Perfect score: 1287  
Sequence: 1 GLDTSVSTKGTATYTYNPF.....AVDQVKPKALKFKVDKDPK 251

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	316	2 JT0753	rRNA N-glycosidase
2	348.5	27.1	245	2 JC4840	rRNA N-glycosidase
3	346	26.9	286	2 S25560	rRNA N-glycosidase
4	343	26.7	576	1 RLQSD	ricin D precursor
5	341	26.5	286	2 JC4235	rRNA N-glycosidase
6	334.5	26.0	564	1 RLCSAG	agglutinin precursor
7	333.5	25.9	527	2 S32430	abrin-b precursor
8	330.5	25.7	294	2 S28421	rRNA N-glycosidase
9	329	25.6	251	2 C39761	abrin (clone 7.2)
10	325	25.3	313	2 S17757	rRNA N-glycosidase
11	321	24.9	289	1 RL7ET	rRNA N-glycosidase
12	320	24.9	528	1 TLZSA	abrin-a precursor
13	315	24.5	247	2 JU0393	karasurin - Mongol
14	315	24.5	289	2 JCS606	karasurin C - Tric
15	311.5	24.2	261	2 JEO401	antiviral protein
16	310	24.1	247	2 JC5032	karasurin-B - Tric
17	306.5	23.8	277	2 S22494	rRNA N-glycosidase
18	300.5	23.3	254	2 PD0018	mistletoe lectin I
19	298	23.2	528	2 S32431	abrin-d precursor
20	298	23.2	562	2 S16022	abrin-c precursor
21	291	22.6	286	1 RLPU6G	rRNA N-glycosidase
22	287.5	22.3	570	2 S62627	agglutinin I precu
23	283.5	22.0	278	2 S23519	beta-luffin - smoo
24	270	21.0	250	2 JN0108	luffin-b - smoo
25	215.5	16.7	278	2 A39817	rRNA N-glycosidase
26	210	16.3	272	2 JC4811	betavulgin - beet
27	202	15.7	310	2 S46239	ribosome-inactivat
28	195	15.2	40	2 S17574	rRNA N-glycosidase
29	181.5	14.1	253	2 S28542	rRNA N-glycosidase

30	181.5	14.1	292	1 RLQHG2	rRNA N-glycosidase
31	181	14.1	289	2 T12573	rRNA N-glycosidase
32	179	13.9	293	2 S17519	rRNA N-glycosidase
33	177.5	13.8	283	2 S05205	rRNA N-glycosidase
34	176.5	13.7	253	2 S28541	rRNA N-glycosidase
35	176.5	13.7	253	2 S28539	rRNA N-glycosidase
36	176.5	13.7	253	2 S29931	rRNA N-glycosidase
37	171.5	13.3	253	2 A58923	rRNA N-glycosidase
38	149	11.6	236	2 S17932	rRNA N-glycosidase
39	121	9.4	106	2 B39761	abrin (clone 3.7)
40	120.5	9.4	1948	2 B69511	N conserved hypoch
41	114.5	8.9	275	2 S33631	tritin - wheat
42	113.5	8.8	280	1 RL6H	rRNA N-glycosidase
43	104.5	8.1	281	2 B38664	30K ribosome inact
44	103	8.0	280	2 JCS848	protein synthesis
45	102.5	8.0	456	2 T05612	hypothetical prote

ALIGNMENTS

RESULT 1  
JT0753

rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum  
N:Alternate names: gelonin; type I ribosome-inactivating protein  
C:Species: Gelonium multiflorum  
C>Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: JT0753; S16489  
R:Nolan, P.A.; Garrison, D.A.; Better, M.  
Gene 134, 223-227, 1993  
A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating prot  
A:Reference number: JT0753; MUID:94085781; PMID:7916721  
A:Accession: JT0753  
A:Molecule type: mRNA  
A:Residues: 1-316 <NOL>  
A:Cross-references: UNIPROT:P33186; UNIPARC:UPI0000133948; GB:L12243; NID:9388633; PDB:1  
R:Motecucchi, P.C.; Lazarini, A.M.; Barbieri, L.; Stripe, F.; Sorla, M.; Lappi, D.  
Int. J. Pept. Protein Res. 33, 263-267, 1989  
A:Title: N-terminal sequence of some ribosome-inactivating proteins.  
A:Reference number: S16331; MUID:89326691; PMID:2753596  
A:Accession: S16489  
A:Molecule type: protein  
A:Residues: 47-89, 'K', '91-92, 'D' <MON>  
A:Cross-references: UNIPARC:UPI0000177F26  
C:Function:  
A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase  
F:1-46/Domain: signal sequence #status predicted <SIG>  
F:47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>  
F:53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 100.0%; Score 1287; DB 2; Length 316;  
Best Local Similarity 100.0%; Pred. No. 1.3e-100;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGTATYTYNPNFLNRLVKLPKGNHGIPLLRKCKDDPKCFVLVALSNDN 60  
DB 47 GLDTSVSTKGTATYTYNPNFLNRLVKLPKGNHGIPLLRKCKDDPKCFVLVALSNDN 106

QY 61 GOLAEIAIDVTSVTVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSEGEK 120  
DB 107 GOLAEIAIDVTSVTVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSEGEK 166

QY 121 AYRTTDLGIEPLRIGIKLDENADINYPTEIASSLLVWQVSEARPFPIENQIRNN 180  
DB 167 AYRTTDLGIEPLRIGIKLDENADINYPTEIASSLLVWQVSEARPFPIENQIRNN 226

QY 181 FQQRIRPANNTISLENKWKLSFOIRTSANGMFSSEAVELERANGKKYVTVAVDQVKPKI 240  
DB 227 FQQRIRPANNTISLENKWKLSFOIRTSANGMFSSEAVELERANGKKYVTVAVDQVKPKI 286

QY 241 ALLKFPVDKDPK 251





J. Biol. Chem. 260, 15682-15686, 1985  
A>Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
A/Reference number: A24261; MUID:86059449; PMID:2999130  
A/Accession: A24261  
A/Molecule type: mRNA  
A/Residues: 1-564 <RNA>  
A/Cross-references: UNIPROT:P06750; UNIPARC:UPI0000125689; GB:M12089; NID:g169700; PIDN:  
R:Araki, T.; Yoshioaka, Y.; Funatsu, G.  
Biochim. Biophys. Acta 872, 277-285, 1986  
A>Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti  
A/Reference number: A24210  
A/Accession: A24210  
A/Molecule type: protein  
A/Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-  
A/Cross-references: UNIPARC:UPI0000174679  
A/Comment: This protein has strong agglutinating activity and weak cytotoxicity compared  
C:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-290/Product: agglutinin chain A #status predicted <ACH>  
F:35-281/Domain: rRNA N-glycosidase homology <RNG>  
F:303-564/Product: agglutinin chain B #status experimental <BCH>  
F:319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats  
F:34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:200,203/Active site: Glu, Arg #status predicted  
F:282-306,322-342,453-466,492-509/Disulfide bonds: #status predicted  
F:324,337,348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted  
F:397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 26.0%; Score 334.5; DB 1; Length 564;  
Best Local Similarity 36.3%; Pred. No. 3.2e-20;  
Matches 91; Conservative 42; Mismatches 105; Indels 13; Gaps 7;  
QY 5 VPSFTKGATYYTYVNFLELAVKLPKGN-SHGIPLLRKKCDP-GKCFVLVALSNDNGQ 62  
DB 33 INFTTADATVSYTYTFIRAVRSHLTGTGADVRHIEVLPNRVGLPISQRFILVELSNHAE 92  
QY 63 LAEIAIDVTSVVVGVQVNRNSYFFKADP-----AAVEGLFKNTIKT-RLHFSGSYPSL 116  
DB 93 SVTLALDVNAVVCGRAGNSAYFFH--PDNQEDAEATHLFTDVQNSFTFAFGGNYDEL 150  
QY 117 EGKAYRETTDLGIEPLRIGIKKLDENADINYPKEIASLLVVIQMVSEAAARFTFIENQ 176  
DB 151 EQLGGLRENIELGTGLEDALSYSTCGTQIPTLARSFVVCIMISEAARFOYIERGE 210  
QY 177 IRN--NFQOIRPANNTISLENKWKLSFQIRTSANGMSEAVELERANGKYYVTAVD 234  
DB 211 MKRTRYNRRSAPDPSVITLNSWGLSTAIQESN-QGAFASPIQLQRRNGSKFNVDVS 269  
QY 235 QVKPKIALKLF 245  
DB 270 ILIPIALVMVY 280

RESULT 7  
S32430  
N:Contains: - Indian licorice (fragment)  
C:Species: Abrus precatorius (Indian licorice)  
C/Date: 30-Sep-1993 #sequence revision 01-Aug-1997 #text\_change 09-Jul-2004  
A/Accession: S32430; JCI1399  
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
J. Mol. Biol. 229, 263-267, 1993  
A>Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing. Co  
A/Reference number: S32429; MUID:93132798; PMID:8421313  
A/Accession: S32430  
A/Molecule type: mRNA  
A/Residues: 1-527 <HUN>  
A/Cross-references: UNIPROT:Q06077; UNIPARC:UPI0000125160; GB:M98345; NID:g166296; PIDN:  
R:Kimura, M.; Sumizawa, T.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 57, 166-169, 1993

A>Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic  
A/Reference number: JCI1398; MUID:93169023; PMID:7763422  
A/Accession: JCI1399  
A/Molecule type: protein  
A/Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430  
A/Cross-references: UNIPARC:UPI0000177F2A  
A/Experimental source: seed  
A:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p  
F:1-250/Product: abrin-b chain A #status predicted <ACH>  
F:7-245/Domain: rRNA N-glycosidase homology <RNG>  
F:260-527/Product: abrin-b chain B #status experimental <BCH>  
F:282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
F:714,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:163,166/Active site: Glu, Arg #status predicted  
F:246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted  
F:287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
F:499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 25.9%; Score 333.5; DB 2; Length 527;  
Best Local Similarity 37.7%; Pred. No. 3.5e-20;  
Matches 97; Conservative 34; Mismatches 103; Indels 23; Gaps 9;  
QY 5 VPSFTKGATYYTYVNFLELAVKLPKGN-SHGIPLLRKKCDPDKC-----FVLVALSND 59  
DB 5 IKFTTEGATSQYKQFTEALRQL-TGGLIHGIVL-----PDPTTLOERNYIISVELSNS 59  
QY 60 NGQLAETAIDVTSVVVGVQVNRNSYFFKADPDAAYEGLPKNTIKTRLHFSGSYPSLEG- 118  
DB 60 DTSIEAGIDVSNAYVAYRAGNSYFLRDAPTASRYLFTGTQOYSLRFGNSYIDLRL 119  
QY 119 EKAYRETTDLGIEPLRIGIKKLDENADINYPKEIASLLVVIQMVSEAAARFTFIENQ-- 176  
DB 120 ARQTRQOPIPLGLQALRHAIPLQSGTDQ----EIARTLIVIIQWSEAAARFYISYRVG 175  
QY 177 --IRNNFQOIRPANNTISLENKWKLSFQIRTSANGMSEAVELERANGKYYVTAV- 233  
DB 176 VSIRTN--TAFQPDAAIMISLENNWDNLGGVQQS--VODTFPNAVTLRSVNNQPIVDSLT 232  
QY 234 DOVKPKIALKFVDKDP 250  
DB 233 HQSVAVLALMFLVCNPP 249

RESULT 8  
S28421  
rRNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed  
N/Alternate names: antiviral protein alpha-PAP  
C/Species: Phytolacca americana (Virginian pokeweed)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
A/Accession: S28421  
R:Kataoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koiwai, A.  
Plant Mol. Biol. 20, 879-886, 1992  
A>Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein  
A/Reference number: S28421; MUID:93099240; PMID:1281438  
A/Accession: S28421  
A/Molecule type: DNA  
A/Residues: 1-294 <KAT>  
A/Cross-references: UNIPROT:Q03464; UNIPARC:UPI0000133946; EMBL:D10600; NID:g218010; PID  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: Glycosidase; hydrolase  
F:30-278/Domain: rRNA N-glycosidase homology <RNG>

Query Match 25.7%; Score 330.5; DB 2; Length 294;  
Best Local Similarity 32.2%; Pred. No. 2.9e-20;  
Matches 85; Conservative 50; Mismatches 102; Indels 27; Gaps 8;  
QY 2 LDTVTSFTKGATYYTYVNFLELAVKLPKGN-SHGIPLLRKKCDPDKCFVLVALSNDN 60  
DB 25 INTITFDVGNATINKYATFMKSIHQAKDPTLKCVCIPMLPNTNLTPK--YLLVTLQDSS 82



QY 61 GQLAIAIDVTSVYVVG-----YQVNRSYFFKDAADAAVEGLFKWTIKTRL----- 107  
Db 83 LKTIITMLKRNLLYVYGADTYNGKCRVHPKDISNTTE-----RNDVMTLCPNPSSRVG 138  
QY 108 ---HFGGSPSLEGKAY-RETTDLGIEPLRIGIKKLDENALDNYKPTETIASLLAVIQM 163  
Db 139 KNINDSSYPALKKKVGRPSQVQIGIQLNSGIGKI--YGVDSFTKTEAEFLVALQIM 196  
QY 164 VSEAAARFTFIEQIRNNFQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELE 223  
Db 197 VSEAAARFKYIENQVNTFNRAFPNAPKVLNLEESGKISTAIH-NAKNGALTSPLKNA 255  
QY 224 NGKKYVTVAVDQVKPAILKKVD 247  
Db 256 NGSKWILVRVDDIEBPDVGLLKYVN 279  
RESULT 9  
C39761  
abrin (clone 7.2) precursor - Indian licorice (fragment)  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Abrus precatorius (Indian licorice)  
C:Date: 21-Feb-1992 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: C39761; S14471  
R:Evansen, G.; Mathiesen, A.; Sundan, A.  
J. Biol. Chem. 266, 6848-6852, 1991  
A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
A:Reference number: A39761; MUID:91201329; PMID:2016300  
A:Accession: C39761  
A:Molecule type: DNA  
A:Residues: 1-251 <EVZ>  
A:Cross-references: UNIPROT:Q38760; UNIPARC:UPI0000177P2F  
R:Evansen, G.; Mathiesen, A.; Sundan, A.  
submitted to the EMBL Data Library, October 1990  
A:Description: Direct molecular cloning of two distinct abrin A-chains.  
A:Reference number: S14471  
A:Accession: S14471  
A:Molecule type: DNA  
A:Residues: 'M', 1-251 <EVZ>  
A:Cross-references: UNIPARC:UPI0000AAB08; EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID  
C:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: duplication; glycosidase; hydrolase; lectin; toxin  
F:1-246/Product: abrin (clone 7.2) chain A #status predicted <ACH>  
F:7-246/Domain: rRNA N-glycosidase homology <RNG>  
F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:164,167/Active site: Glu, Arg #status predicted  
Query Match 25.6%; Score 329; DB 2; Length 251;  
Best Local Similarity 36.5%; Pred. No. 3.1e-20;  
Matches 93; Conservative 40; Mismatches 104; Indels 18; Gaps 8;  
QY 5 VSPSTKGATYITYVNFLELVKLPKGNHGIPLLRKKCDPGKC-----FVLVALSND 59  
Db 5 IKFSTEGATSYKQFIALRERLR-GLLIHDIPVLR----DPTVEERNYITVELSNS 59  
QY 60 NGQLAIAIDVTSVYVVGQVNRNRYFFKDAADAAVEGLFKNTIKRLHFGGSPSLR-G 118  
Db 60 ERESIEVGIDVTNAVVAIRAGSQSYFLRDAPASATVLTCTQYSLRFDGSGYDLERW 119  
QY 119 EKAYRETTDLGIEPLRIGIKKLDENALDNYKPTETIASLLVVIQMVSEAAARFTFIEQIR 178  
Db 120 AHQTEQISLGLQALTHAISPLRSASND---EEKARTLIVIQWASEAARVRYISNRVG 176  
QY 179 NNFQ--QIRPANNTISLENKWKLSFQIRTSANGMFSEAVELEERANGKYYTVAV-DQ 235  
Db 177 VSRITGTAFQPDPAMLSENNDNISRGVQES-VQDTFPNAVTLRVRNNQPVIVDSLTHQ 235  
QY 236 VKPKIALLKFDKOP 250  
Db 236 SVAVLALMLFVGNPP 250

RESULT 10

S17757  
rRNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed  
N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-in-  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: S17757; S02792; S13469; S32611  
R:Lin, Q.; Chen, Z.C.; Antoniw, J.F.; White, R.F.  
Plant Mol. Biol. 17, 609-614, 1991  
A:Title: Isolation and characterization of a cDNA clone encoding the anti-viral protein  
A:Reference number: S17757; MUID:92003676; PMID:1912488  
A:Accession: S17757  
A:Molecule type: DNA  
A:Residues: 1-313 <LIN>  
A:Cross-references: UNIPROT:P10297; UNIPARC:UPI0000133932; EMBL:X55383; NID:g20421; PIDN  
R:Barbieri, L.; Bolognesi, A.; Cenini, P.; Falasca, A.I.; Minghetti, A.; Garofano, L.;  
Biochem. J. 257, 801-807, 1989  
A:Title: Ribosome-inactivating proteins from plant cells in culture.  
A:Reference number: S02792; MUID:89193489; PMID:2930487  
A:Accession: S02792  
A:Molecule type: protein  
A:Residues: 23-55, 'X', 57-65 <BAR>  
A:Cross-references: UNIPARC:UPI0000177P24  
R:Bolognesi, A.; Barbieri, L.; Abbondanza, A.; Falasca, A.I.; Carnicelli, D.; Battelli,  
Biochim. Biophys. Acta 1087, 293-302, 1990  
A:Title: Purification and properties of new ribosome-inactivating proteins with RNA N-g  
A:Reference number: S13469; MUID:91064383; PMID:2248976  
A:Accession: S13469  
A:Molecule type: protein  
A:Residues: 23-54 <BOI>  
A:Cross-references: UNIPARC:UPI0000177P25  
R:BJorn, M.J.; Larrick, J.; Piatak, M.; Wilson, K.J.  
Biochim. Biophys. Acta 790, 154-163, 1984  
A:Title: Characterization of translational inhibitors from Phytolacca americana. Amino-t  
A:Reference number: S32610; MUID:85023392; PMID:6091760  
A:Accession: S32611  
A:Molecule type: protein  
A:Residues: 23-54 <BJO>  
A:Cross-references: UNIPARC:UPI0000177P25  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-313/Product: rRNA N-glycosidase PAP #status experimental <MAT>  
F:28-277/Domain: rRNA N-glycosidase homology <RNG>  
Query Match 25.3%; Score 325; DB 2; Length 313;  
Best Local Similarity 31.6%; Pred. No. 9.1e-20;  
Matches 84; Conservative 49; Mismatches 101; Indels 32; Gaps 8;  
QY 2 LDTVSFSTKGATYITYVNFLELVKLPK-PEGNSHGIPLLRKKDDPGKCFVLVALSNDN 60  
Db 23 VNTIIVNGVSTTISKYATFLNLRNEAKDPSLKCVCIGIPMLPNTNPK--YVLVELQGSN 80  
QY 61 GQLAIAIDVTSVYVVGQ-----VNRNRYFFKDAADAAVEGLFKNT 102  
Db 81 KKTITLRLRNLLYVVGSDPPFTNCKRYHFNDSIGTERQDVTTLCPNA-----NSR 134  
QY 103 IKTLHFGGSPSLEGKAY--RETTDLGIEPLRIGIKKLDENALDNYKPTETIASLLAV 160  
Db 135 VSKNINDSRPTIESKAGVKSQVQIGIQLNSGIGKI--SGVMSSTKTEAEFLVA 192  
QY 161 IQMVSEAAARFTFIEQIRNNFQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVE 220  
Db 193 IQMVSEAAARPKYIENQVNTFNRAFPNAPKVLNLEQETWGIKISTAIH-DAKNGVLPKPLEL 251  
QY 221 ERANGKYYTVAVDQVKPAILKKFV 246  
Db 252 VDASGAKWILVRVDEIKPDVALLNV 277  
RESULT 11  
RUTZT  
rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian s  
N:Alternate names: alpha-TCS; type I ribosome-inactivating protein

F;93,193,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 24.9%; Score 321; DB 1; Length 289;  
Best Local Similarity 37.8%; Pred. No. 1.8e-19;  
Matches 93; Conservative 35; Mismatches 104; Indels 14; Gaps 8;

Qy 5 VSFSTKGATYITVNFNLRLVKLPKPGNSHGIPLLRKKCDPQ-KCFVLVALSNDNGQL 63  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 25 VSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSL--PGSQRYALIHLTNYADET 82  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Qy 64 AETAIDVTSVVVGVQVRNRSYEFKDA-PDAAVEGLFKNTI-KTRLHFGGSYPSLE-GEK 120  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 83 ISVAIDVTNVIINGYRAGDTSYFNFNSASATEAAKYVFKQAMRKVTLPISNGYERLQTAAG 142  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Qy 121 AVRETTDLGTEPIRIGIKKLDENAIQNYKPTETIASLLVVVIQWVSAARFTFIENQIRNN 180  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 143 KIRENIPGLGALDSAI-----TTLFYVNSAASALMWLIQSTSEARAYKFFIEQIGKR 197  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Qy 181 FQRIIRPANNWISLENKWKLSFQIR-TSGANGWFSEAVELEPRANGKYYVTVADQ--VK 237  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 198 VDKTFLPSLAIIISLENSWSALSQKIQTASTNNGQFSPVVLINAQNRVTITNVDAGVVT 257  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Qy 238 PKTALL 243  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 258 SNTALL 263  
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 12

TLJSA

abrin-a precursor - Indian licorice (fragment)  
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C;Species: Abrus precatorius (Indian licorice)  
C;Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text change 09-Jul-2004  
C;Accession: S32429, J70202; A39761; JCI398, S14472; S24133; S74110; S74111  
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
J. Mol. Biol. 229, 263-267, 1993  
A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing  
A;Reference number: S32429; MUID:93132798; PMID:8421313  
A;Accession: S32429  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 'E', 2-528 <HUN>  
A;Cross-references: UNIPROT:P11140; UNIPARC:UPI000016DA00; GB:M98344; NID:g1662  
A;Note: the coding region for the sequence shown is preceded by an ATG codon  
A;Note: residues 1-8 were derived from the synthesized primer  
R;Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.  
Agric. Biol. Chem. 52, 1095-1097, 1988  
A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein  
A;Reference number: J70202  
A;Accession: J70202  
A;Molecule type: protein  
A;Residues: 1-201,203-251 <FUN>  
A;Cross-references: UNIPARC:UPI000017467A  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore  
R;Evensen, G.; Mathiesen, A.; Sundan, A.  
J. Biol. Chem. 266, 6848-6852, 1991  
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains  
A;Reference number: A39761; MUID:91201329; PMID:2016300  
A;Accession: A39761  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 'E', 2-251 <EVE>  
A;Cross-references: UNIPARC:UPI000011046A; GB:X54872  
R;Note: residues 1-8 were derived from the synthesized primer  
R;Kimura, M.; Sumizawa, T.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 57, 166-169, 1993  
A;Title: The complete amino acid sequences of the B-chains of abrin-a and abrin-b  
A;Reference number: JCI398; MUID:93169023; PMID:7763422  
A;Contents: seeds  
A;Accession: JCI398  
A;Molecule type: protein  
A;Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>  
A;Cross-references: UNIPARC:UPI000017467B





GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:39:04 ; Search time 12.9668 Seconds  
(without alignments)  
254.015 Million cell updates/sec

Title: US-10-717-243-2

Perfect score: 1287

Sequence: 1 GLDVTVSFTKGATYTYNFF.....AVDQVKPKIALKFVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US08 NEW PUB.pap.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US06 NEW PUB.pap.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US07 NEW PUB.pap.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB.pap.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US03 NEW PUB.pap.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US10 NEW PUB.pap.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US11 NEW PUB.pap.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US60 NEW PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343	26.7	268	7 US-11-010-795-24	Sequence 24, Appl
2	343	26.7	576	6 US-10-923-022-1	Sequence 1, Appli
3	343	26.7	630	6 US-10-893-584-274	Sequence 274, App
4	325	25.3	313	7 US-11-010-795-20	Sequence 20, Appl
5	307	23.9	267	6 US-10-517-707A-1	Sequence 1, Appli
6	246.5	19.2	190	6 US-10-923-022-11	Sequence 11, Appl
7	245.5	19.1	200	6 US-10-923-022-10	Sequence 10, Appl
8	243.5	18.9	188	6 US-10-923-022-4	Sequence 4, Appli
9	243.5	18.9	188	6 US-10-923-022-8	Sequence 8, Appli
10	243.5	18.9	189	6 US-10-923-022-6	Sequence 6, Appli
11	242.5	18.8	198	6 US-10-923-022-3	Sequence 3, Appli
12	242.5	18.8	198	6 US-10-923-022-7	Sequence 7, Appli
13	242.5	18.8	199	6 US-10-923-022-5	Sequence 5, Appli
14	240	18.6	267	6 US-10-517-707A-7	Sequence 7, Appli
15	239	18.6	185	6 US-10-923-022-9	Sequence 9, Appli
16	202	15.7	310	7 US-11-010-795-22	Sequence 22, Appl
17	173.5	13.5	179	6 US-10-923-022-2	Sequence 2, Appli
18	83.5	6.5	315	7 US-11-010-795-28	Sequence 28, Appl
19	83	6.4	319	7 US-11-010-795-26	Sequence 26, Appl
20	82.5	6.4	1183	7 US-11-115-639-13	Sequence 13, Appl
21	82.5	6.4	1183	7 US-11-115-639-14	Sequence 14, Appl
22	82.5	6.4	1183	7 US-11-115-639-15	Sequence 15, Appl
23	82.5	6.4	1183	7 US-11-115-639-16	Sequence 16, Appl
24	82.5	6.4	1183	7 US-11-115-639-17	Sequence 17, Appl
25	82.5	6.4	1183	7 US-11-115-639-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-11-010-795-24  
; Sequence 24, Application US/11010795  
; Publication No. US20060005271A1  
; GENERAL INFORMATION:  
; APPLICANT: TUMER, NILGUN E.  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE  
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS  
; FILE REFERENCE: OCIRS 3.0-085  
; CURRENT APPLICATION NUMBER: US/11/010,795  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: 60/529,348  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: Patent In Ver. 3.3  
; SEQ ID NO 24  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-11-010-795-24

Query Match 26.7%; Score 343; DB 7; Length 268;  
Best Local Similarity 36.8%; Pred. No. 4.8e-25;  
Matches 93; Conservative 45; Mismatches 99; Indels 16; Gaps 9;

QY 5 VSFSTKGNATYTYNFFLNELRVKLKPEGN-SHGIPLLRKKCCDDP-GKCFVLVALSNDNGQ 62  
DB 10 INFNTAGATQVSYTNFTRAVRGRLTTGADVRIPEVLPNVRVGLPNQRPFILVLSNHAEL 69  
QY 63 LAETAIIDVTSYVVGQYQVRNRSYFFKADPD-----AAVEGLFKNTIKTR--LHFGGSYPS 115  
DB 70 SVTLALDVTNAYVVGVRAGNSAYFFH--PDNQEDAEALTHLFTD-VQRYTFAGGNYDR 126  
QY 116 LEGEKA-YRETTDGIIEPLRIGIKKL DENAIDNYKPTBIASLLVVIQMVSEAAFTPIE 174  
DB 127 LEQLAGNLRENIELGNGLPEBAISALYYSTGTQPLTLARSFFIICIMSEAAFPQVIE 186  
QY 175 NQIRN--NFQOIRIPANNITISLENKWKGLSQIRTSANGHMFSEAVELERANGKYYTA 232  
DB 187 GEMTRIRYNRSAPDPFSVITLNSWGLRSLTAIQESN--QGAFASPIQLQRNGSKFSYVD 245  
QY 233 VDQVKPKIALKF 245  
DB 246 VSLIPIIALMVY 258

RESULT 2



Db 252 VDASGAKWIVLRVDEIKPDVALLNV 277

# RESULT 5

US-10-517-707A-1

; Sequence 1, Application US/10517707A

; Publication No. US20060019885A1

; GENERAL INFORMATION:

; APPLICANT: BAKER, Matthew

; APPLICANT: CARE, Francis J.

; TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED

; FILE REFERENCE: MER-134

; CURRENT APPLICATION NUMBER: US/10/517,707A

; PRIOR FILING DATE: 2004-12-10

; PRIOR APPLICATION NUMBER: PCT/EP03/06055

; PRIOR FILING DATE: 2003-06-10

; PRIOR APPLICATION NUMBER: EP 02012911.0

; PRIOR FILING DATE: 2002-06-11

; NUMBER OF SEQ ID NOS: 183

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-517-707A-1

Query Match 23.9%; Score 307; DB 6; Length 267;

Best Local Similarity 36.3%; Pred. No. 1.2e-21;

Matches 89; Conservative 36; Mismatches 108; Indels 12; Gaps 7;

QY 5 VSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDNGOLA 64

DB 2 VSFRLSGATTSYGVFIKNLREALPVRKVYNIPLRSSISGSR-YTLHLHTYADETI 60

QY 65 EIAIDVTSVYVGVQVRNRSYFFKDA-PDAAYEGLFKWT-INTRLHFGSGYPSLE-GEKA 121

DB 61 SVAVDTNVMYINGYLADGVSYPFNEASATEAAKVFYKDAKKVTLFYSNGYERLQTAAGK 120

QY 122 YRETTDLGIEPLRIGIKKLDENAIQKPTETASSLLVVIQMVSEARFTPIENQIRNF 181

DB 121 IRENPLGLPALDSAI-----TTLTYTASSAASALLVLIQSTAESARYKFTIEQIGKRV 175

QY 182 QORIRPANNTISLENKWKLSFQIR-TSGANGMFSEAVELELRANGKTYVT--AVDQVKP 238

DB 176 DKTEPLSLATISLENNWSALSQIQIASTNNQFSPVVLIDENNQRYSITNASARVTS 235

QY 239 KIALI 243

DB 236 NIALI 240

# RESULT 6

US-10-923-022-11

; Sequence 11, Application US/10923022

; Publication No. US20060009619A1

; GENERAL INFORMATION:

; APPLICANT: Olson, Mark A

; APPLICANT: Millard, Charles B

; APPLICANT: Byrnes, Michael P

; APPLICANT: Wannemacher, Robert W

; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

; FILE REFERENCE: P67452US0 (RIID 01-58)

; CURRENT APPLICATION NUMBER: US/10/923,022

; CURRENT FILING DATE: 2004-08-23

; PRIOR APPLICATION NUMBER: US/10/083,336

; PRIOR FILING DATE: 2002-02-27

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 190

; TYPE: PRT

; ORGANISM: Ricinus communis

US-10-923-022-11

Query Match

Best Local Similarity 19.2%; Score 246.5; DB 6; Length 190;

Matches 68; Conservative 32; Mismatches 73; Indels 19; Gaps 6;

QY 5 VSFSTKGATYTYVNFNLRLVRLKPEGNHGIPLLRKKDDPGKCFVLVALSNDNGOLA 64

DB 10 INFTTAGATVQSYTNFIRAVGRLLTVLPNRVGLPINQR-----FILVELSNHAEISV 61

QY 65 EIAIDVTSVYVGVQVRNRSYFFKDA-PD-----AYEGLFKNTIKTR--LHFGGSYPSLE 117

DB 62 TLALDVTNAYVVGVRAGNSAYFFH--PDNQSDAEATHTLFTD-VQNRVTFAPGGYDRLE 118

QY 118 GEKA-YRETTDLGIEPLRIGIKKLDENAIQKPTETASSLLVVIQMVSEARFTPIENQ 176

DB 119 QLAGNLRNIEIENGCPLEASALYYSTGTQPLTLARSPFIQIOMISEARFOYIRGE 178

QY 177 IRNNFQQRIRPA 188

DB 179 MRTRIRYNRRA 190

# RESULT 7

US-10-923-022-10

; Sequence 10, Application US/10923022

; Publication No. US20060009619A1

; GENERAL INFORMATION:

; APPLICANT: Olson, Mark A

; APPLICANT: Millard, Charles B

; APPLICANT: Byrnes, Michael P

; APPLICANT: Wannemacher, Robert W

; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

; FILE REFERENCE: P67452US0 (RIID 01-58)

; CURRENT APPLICATION NUMBER: US/10/923,022

; CURRENT FILING DATE: 2004-08-23

; PRIOR APPLICATION NUMBER: US/10/083,336

; PRIOR FILING DATE: 2002-02-27

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 200

; TYPE: PRT

; ORGANISM: Ricinus communis

US-10-923-022-10

Query Match

Best Local Similarity 19.1%; Score 245.5; DB 6; Length 200;

Matches 70; Conservative 32; Mismatches 79; Indels 13; Gaps 7;

QY 5 VSFSTKGATYTYVNFNLRLVRLKPEGN-SHGIPLLRKKDDP-GKCFVLVALSNDNGQ 62

DB 10 INFTTAGATVQSYTNFIRAVGRLLTVGADVREHFPVLPNRVGLPINQRFILVELSNHAEI 69

QY 63 LAEIAIDVTSVYVGVQVRNRSYFFKDA-PD-----AAYEGLFKNTIKTR--LHFGGSYPS 115

DB 70 SVTLALDVTNAYVVGVRAGNSAYFFH--PDNQSDAEATHTLFTD-VQNRVTFAPGGYDR 126

QY 116 LEGEKA-YRETTDLGIEPLRIGIKKLDENAIQKPTETASSLLVVIQMVSEARFTPIE 174

DB 127 LEQAGNLRNIEIENGCPLEASALYYSTGTQPLTLARSPFIQIOMISEARFOYIRGE 186

QY 175 NOIRNNFQQRIRPA 188

DB 187 GEMETRIRYNRRA 200

# RESULT 8

US-10-923-022-4

; Sequence 4, Application US/10923022

; Publication No. US20060009619A1

; GENERAL INFORMATION:

; APPLICANT: Olson, Mark A





```
; ORGANISM: Ricinus communis
US-10-923-022-3

Query Match      18.8%; Score 242.5; DB 6; Length 198;
Best Local Similarity 37.0%; Pred. No. 8.8e-16;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

QY 5 VSPSTKGATYTYVNFNLRLVRLKPEGN-SHGIPLLRKKCDP-GKCFVLVALSNDNGQ 62
Db 9 INFTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRVGLPQNPQFVLVLSNHAEL 68
QY 63 LAEIAIDVTSVVVGVQVNRNSYFFPKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
Db 69 SVTLALDVTVNAVVGVRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYTFAFGNYDR 125
QY 116 LEGEKA-YRETTDLGIEPIRGIKKLDENADINYPKTEIASLLVVIQMVSEAAARPTFIE 174
Db 126 LEQLAGNLRENIELGNGPLEBAISALYYSTGGTQPLTARSFIICQWISAAARFQVIE 185
QY 175 NOIRNNFOQIR 186
Db 186 GEMRT----RIR 193

RESULT 12
US-10-923-022-7
; Sequence 7, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-7

Query Match      18.8%; Score 242.5; DB 6; Length 198;
Best Local Similarity 37.0%; Pred. No. 8.8e-16;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

QY 5 VSPSTKGATYTYVNFNLRLVRLKPEGN-SHGIPLLRKKCDP-GKCFVLVALSNDNGQ 62
Db 9 INFTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRVGLPQNPQFVLVLSNHAEL 68
QY 63 LAEIAIDVTSVVVGVQVNRNSYFFPKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
Db 69 SVTLALDVTVNAVVGVRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYTFAFGNYDR 125
QY 116 LEGEKA-YRETTDLGIEPIRGIKKLDENADINYPKTEIASLLVVIQMVSEAAARPTFIE 174
Db 126 LEQLAGNLRENIELGNGPLEBAISALYYSTGGTQPLTARSFIICQWISAAARFQVIE 185
QY 175 NOIRNNFOQIR 186
Db 186 GEMRT----RIR 193

RESULT 13
US-10-923-022-5
; Sequence 5, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-5

Query Match      18.8%; Score 242.5; DB 6; Length 199;
Best Local Similarity 37.0%; Pred. No. 8.9e-16;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

QY 5 VSPSTKGATYTYVNFNLRLVRLKPEGN-SHGIPLLRKKCDP-GKCFVLVALSNDNGQ 62
Db 10 INFTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRVGLPQNPQFVLVLSNHAEL 69
QY 63 LAEIAIDVTSVVVGVQVNRNSYFFPKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
Db 70 SVTLALDVTVNAVVGVRAGNSAYFFH--PDNQEDAEATHLFTD-VQNYTFAFGNYDR 126
QY 116 LEGEKA-YRETTDLGIEPIRGIKKLDENADINYPKTEIASLLVVIQMVSEAAARPTFIE 174
Db 127 LEQLAGNLRENIELGNGPLEBAISALYYSTGGTQPLTARSFIICQWISAAARFQVIE 186
QY 175 NOIRNNFOQIR 186
Db 187 GEMRT----RIR 194

RESULT 14
US-10-517-707A-7
; Sequence 7, Application US/10517707A
; Publication No. US20060019885A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
; FILE REFERENCE: MER-134
; TITLE OF INVENTION: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/517,707A
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06055
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: EP 02012911.0
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified byrodin 1 protein
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 48, 49, 51, 54
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Met, Ala, Gly, Pro, Ile
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Pro, Tyr
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: 55, 60, 64, 66
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```

; OTHER INFORMATION: Xaa=Thr, Ser
; OTHER INFORMATION: Xaa=Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 94, 95, 103, 114
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, His, Asp, Glu, Asn, Gln, Lys,
; OTHER INFORMATION: Arg, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Pro, Ser, Thr, His, Lys
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 117, 119, 120, 121
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=His
; OTHER INFORMATION: Xaa=Ser
; OTHER INFORMATION: Xaa=Ala, Ser, thr, Pro, Asn, Asp, Glu, Gly, His,
; OTHER INFORMATION: Lys, Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 122, 125, 139, 132
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=Ala, Pro
; OTHER INFORMATION: Xaa=Ala, Ile, Phe, Gly, Met, Pro, Val, Trp, Tyr
; OTHER INFORMATION: Xaa=Phe, Pro, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137) ... (143)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (152) ... (155)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ile, Met, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr, His, Asp, Asn, Gln,
; OTHER INFORMATION: Lys, Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (187) ... (198)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Gln
; OTHER INFORMATION: Xaa=His, Lys, Arg, Asp, Glu, Asn,, Phe, Leu, Pro,
; OTHER INFORMATION: Ser, Tyr, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (200) ... (202)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Asp
; US-10-517-707A-7
Query Match      18.6%; Score 240; DB 6; Length 267;
Best Local Similarity 30.5%; Pred. No. 2.3e-15;
Matches 75; Conservative 33; Mismatches 124; Indels 14; Gaps 7
Qy 5 VSFSTKGATITYYNFLNELRVKLKPEGNHSHGIFLLRKCCDDPGKFVLVALSNDNGQLA 64
Db ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
2 VSPRLSGATTTSYGVFKINLREALPYERKVYNIPLLRSSISGSGR-YXXLMLTXXADETX 60
Qy 65 EIALDVTSVVVVGQVRNSVFPPKDA-PDAAYEGLFKNY-IKTRLHPGSGSYPSLEGEKAY 122
Db 61 SVAXDXTNVYIMGLAGDSVYFNFAASATEAAKKXGFDAKKKXGLTPVSGNY-----BRX 114
Qy 123 RETTDLGIEPLRIGIKKLDENAINDYKPT--EIASSLLVTQMVSSEARFTFIENOIRNN 180

```

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 10.8856 Seconds  
(without alignments)  
807.265 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHNSRVARWASDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: GeneseqP1980s.\*
- 2: GeneseqP1990s.\*
- 3: GeneseqP2000s.\*
- 4: GeneseqP2001s.\*
- 5: GeneseqP2002s.\*
- 6: GeneseqP2003as.\*
- 7: GeneseqP2003bs.\*
- 8: GeneseqP2004s.\*
- 9: GeneseqP2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	2 AAR37300	Aar37300 E.coli sh
2	114	100.0	293	2 AAW58827	Aaw58827 Shiga tox
3	114	100.0	293	2 AAY39393	Aay39393 Shiga-lik
4	114	100.0	293	3 AAY69046	Aay69046 Amino aci
5	114	100.0	315	2 AAW06403	Aaw06403 Verotoxig
6	114	100.0	315	2 AAW21702	Aaw21702 Shiga-lik
7	114	100.0	315	2 AAW25139	Aaw25139 SLT-1 (a
8	114	100.0	315	3 AAY96681	Aay96681 E. coli v
9	114	100.0	315	5 AAU77817	Aau77817 E. coli v
10	114	100.0	315	7 ADC00545	Adc00545 Enterohae
11	114	100.0	315	7 ADH34319	Adh34319 Verotoxin
12	114	100.0	316	2 AAW25786	Aaw25786 Phage H19
13	114	100.0	323	2 AAW06407	Aaw06407 Histidine
14	114	100.0	323	3 AAY96686	Aay96686 Recombina
15	114	100.0	323	5 AAU77822	Aau77822 HIS-tagge
16	114	100.0	326	2 AAW06413	Aaw06413 Flag tag/
17	114	100.0	326	3 AAU96692	Aay96692 FLAG tag/
18	114	100.0	326	5 AAU77828	Aau77828 Flag tag/
19	114	100.0	332	2 AAW29294	Aaw29294 BPI pepti
20	114	100.0	409	2 AAR13118	Aar13118 Shiga-lik
21	114	100.0	409	2 AAY55891	Aay55891 E.coli ba
22	114	100.0	409	3 AAY78591	Aay78591 E. coli b
23	114	100.0	690	3 AAY96694	Aay96694 MBP-VT-1
24	114	100.0	690	5 AAU77830	Aau77830 MBPNVTI-A

25	114	100.0	708	2 AAW06411	Aaw06411 Maltose b
26	114	100.0	708	3 AAY96690	Aay96690 MBP-VT-1
27	114	100.0	708	5 AAU77826	Aau77826 MBPNVTI-A
28	51	44.7	17	9 ADZ89477	Adz89477 Substrate
29	47	41.2	135	7 ADJ68214	Adj68214 Human hea
30	46	40.4	18	9 ADZ89463	Adz89463 Substrate
31	46	40.4	35	7 ADE95989	Ade95989 Human uri
32	46	40.4	35	7 ADK14898	Adk14898 Urinary s
33	46	40.4	196	6 ABU38500	Abu38500 Protein e
34	46	40.4	204	7 ABO69919	AbO69919 Pseudomon
35	45	39.5	19	7 ABR82617	Abr82617 P. aerugi
36	45	39.5	386	3 AAG59236	Agg59236 Arabidops
37	45	39.5	413	6 ADA34573	Ada34573 Acinetoba
38	45	39.5	525	7 ABO79520	AbO79520 Pseudomon
39	44.5	39.0	250	8 ADS21292	AdS21292 Bacterial
40	44.5	39.0	280	8 ADX90199	Adx90199 Plant ful
41	44.5	39.0	544	3 AAB53464	Aab53464 Human col
42	44	38.6	137	4 AAM79060	Aam79060 Human pro
43	44	38.6	137	2 ADJ69294	Adj69294 Human hea
44	44	38.6	138	2 AAW60837	Aaw60837 Human SQM
45	44	38.6	138	5 ABG72567	Abg72567 Human cel

#### ALIGNMENTS

#### RESULT 1

AAAR37300					
XX	AAAR37300	standard; protein; 20 AA.			
AC	AAAR37300;				
XX					
DT	25-MAR-2003	(revised)			
DT	13-SEP-1993	(first entry)			
XX					
DE	E.coli shiga-like toxin segment.				
XX					
KW	Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;				
KW	autoimmune disease; cell killing; toxin; human engineered antibody;				
KW	variable region; light chain; cell targeting; chimeric antibody; SLT.				
XX					
OS	Escherichia coli.				
FH	Key	Location/Qualifiers			
FT	Disulfide-bond	1..20			
FT	/note=	"intervening loop includes protease sensitive			
FT		amino acid sequence"			
XX					
PN	W09309130-A1.				
XX					
PD	13-MAY-1993.				
XX					
PP	04-NOV-1992;	92WO-US009487.			
XX					
PR	04-NOV-1991;	91US-00787567.			
PR	19-JUN-1992;	92US-00901707.			
XX					
PA	(XOMA ) XOMA CORP.				
XX					
PI	Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;				
XX					
DR	WPI, 1993-167617/20.				
XX					
PT	Analogues of type I ribosome inactivating protein - useful as cytotoxic				
PT	agents, immuno toxins for treating autoimmune diseases, cancer, graft				
XX	versus host disease and selective cell killing in-vivo.				
PS	Example 10; Page 114; 163pp; English.				
XX					
CC	The invention covers analogues of the plant type I RIP gelonin which have				
CC	a non-naturally occurring Cys residue in a position which enables the				
CC	analogue to be conjugated via a disulphide linkage to a molecule which				
CC	specifically binds to a target cell. Pref. target-cell binding molecules				

CC are antibodies or their fragments, esp. human engineered H65 antibody  
 CC fragments. Fusion constructs were assembled that included a natural  
 CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an  
 CC H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of  
 CC the E.coli shiga-like toxin was inserted between the gelonin gene and the  
 CC Ab gene. The resulting immunoconjugates can be used as cytotoxic  
 CC therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 20 AA;

Query Match 100.0%; Score 114; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-12;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFFPSMC 20  
 |||||  
 DB 1 CHHHSRVARMSDEFFPSMC 20

RESULT 2  
 AAW58827  
 ID AAW58827 standard; peptide; 293 AA.

AC AAW58827;

DT 18-AUG-1998 (first entry)

DE Shiga toxin type 1 mature A subunit.

KW Histone-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;  
 KW haemorrhagic colitis; haemolytic uremic syndrome.

OS Shigella dysenteriae.

PN WO9811229-A2.

PD 19-MAR-1998.

PF 09-SEP-1997; 97WO-US015836.

PR 10-SEP-1996; 96US-0025637P.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI O'Brien AD, Schmitt CK;

XX WPI; 1998-207390/18.

DR N-PSDB; AAV11400.

XX Purification and isolation of histidine-tagged Shiga toxins - useful in  
 PT vaccines against haemorrhagic colitis and haemolytic uremic syndrome.

PS Claim 1; Fig 2; 47pp; English.

XX The Shiga toxin (Stx) peptides (AAW58827-W58830) were histidine-tagged to  
 CC simplify and expedite purification. Non toxic Shiga toxoids, Fusion  
 CC proteins of His-tagged Shiga toxins/toxoids and antibodies can be used in  
 CC the treatment, diagnosis or prevention of infections mediated by toxins  
 CC of the Stx family. These are associated with haemorrhagic colitis and the  
 CC life-threatening sequelae, haemolytic uremic syndrome. Shiga antibodies  
 CC are also useful for the treatment, diagnosis and prevention of disease  
 CC and infections by pathogenic Escherichia coli

XX Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFFPSMC 20  
 |||||  
 DB 242 CHHHSRVARMSDEFFPSMC 261

RESULT 3  
 AAY39393

ID AAY39393 standard; protein; 293 AA.

AC AAY39393;

DT 20-DEC-1999 (first entry)

DE Shiga-like Toxin 1, A subunit.

KW Shiga toxin; ShT; Shiga-like toxin; SLT; A subunit; B subunit; ricin;  
 KW microorganism clone; combinatorial library; therapeutic protein;  
 KW medicament; target cell; binding specificity.

OS Shigella dysenteriae.

PN WO9940185-A1.

PD 12-AUG-1999.

PF 08-DEC-1998; 98WO-CA001137.

PR 04-FEB-1998; 98CA-02222993.

PA (ONTA-) ONTARIO CANCER INST.

PI Gariepy J, Bray MR;

XX WPI; 1999-590695/50.

XX Production of cytotoxic heteromeric protein combinatorial libraries,  
 PT useful for ability to specifically bind to and kill a target cell.

PS Example 1; Fig 1a; 61pp; English.

XX This is the Shiga-like toxin (SLT) subunit A amino acid sequence. SLT is  
 CC a bacterial toxin related to the Shiga toxin (ShT). SLT and ShT have the  
 CC smallest known B subunit of all AB toxins, and the A subunit has  
 CC identical catalytic activity as the corresponding subunit in ricin. The B  
 CC subunit (AAY39394) is identical for both ShT and SLT. Both the A and B  
 CC subunit amino acid sequences are used in the methods of the invention,  
 CC which relates to the creation of a library of microorganism clones  
 CC producing mutant proteins which are then screened for their ability to  
 CC specifically bind to and kill target cell. AAY39395-Y39389 and AAY3001-  
 CC Y43024 are examples of mutant B subunits identified by the methods of the  
 CC invention. The B subunit of the toxin has high binding specificity, and  
 CC therefore mutant versions of the B subunit may target the toxin to a  
 CC specific cell. Cytotoxic mutant proteins identified by the method can be  
 CC used to identify therapeutic proteins and medicaments having binding  
 CC specificity for a target cell. The cytotoxic mutants can also be used to  
 CC construct diagnostic probes for detecting the presence of cell surface  
 CC markers. These medicaments can be used to target medicines to target  
 CC cells in host organisms

XX Sequence 293 AA;

Query Match 100.0%; Score 114; DB 2; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFFPSMC 20  
 |||||  
 DB 242 CHHHSRVARMSDEFFPSMC 261

RESULT 4  
 AAY69046

ID AAY69046 standard; protein; 293 AA.

AC AAY69046;

DT 30-MAY-2000 (first entry)

XX Amino acid sequence of exemplary cell toxin shiga toxin A-chain.  
 DE  
 XX  
 XX Chemokine receptor; ligand; inflammatory response; immune effector cell;  
 KW secondary tissue damage; central nervous system injury; shiga;  
 KW CNS inflammatory disease; neurodegenerative disorder; heart disease;  
 KW inflammatory eye disease; inflammatory bowel disease; PCR primer;  
 KW inflammatory joint disease; inflammatory kidney; renal disease;  
 KW inflammatory lung disease; inflammatory nasal disease; thyroiditis;  
 KW inflammatory thyroid disease; cytokine-regulated cancer; ss.  
 XX  
 XX Shigella dysenteriae.  
 XX  
 XX WO200004926-A2.  
 XX  
 XX 03-FEB-2000.  
 XX  
 XX 21-JUL-1999; 99WO-CA000659.  
 XX  
 XX 22-JUL-1998; 98US-00120523.  
 XX  
 XX (OSPR-) OSPREY PHARM LTD.  
 XX  
 XX McDonald JR, Coggins RJ;  
 XX  
 XX WPI; 2000-182542/16.  
 XX  
 XX A new therapeutic agent comprising a conjugate for treating secondary  
 PT tissue damage and other disease conditions like Alzheimer's disease,  
 PT stroke, Parkinson's disease and atherosclerosis.  
 XX  
 XX Disclosure; Page 67; 204pp; English.  
 XX  
 XX The present sequence represents an exemplary cell toxin, which can be  
 CC incorporated into the conjugates of the invention. The specification  
 CC describes a conjugate, comprising a targeted agent and a chemokine  
 CC receptor ligand. The conjugate binds to a chemokine receptor resulting in  
 CC internalisation of the targeted agent in cells bearing the receptor. The  
 CC conjugates are used for formulating a medicament or for treating  
 CC disorders associated with inflammatory responses resulting from  
 CC activation, proliferation and migration of immune effector cells. The  
 CC disorders or disease states comprise secondary tissue damage such as  
 CC central nervous system (CNS) injury, CNS inflammatory diseases,  
 CC neurodegenerative disorders, heart disease, inflammatory eye diseases,  
 CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory  
 CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal  
 CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-  
 CC regulated cancers  
 XX  
 XX Sequence 293 AA;  
 Query Match 100.0%; Score 114; DB 3; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0;  
 Qy 1 CHHHSRVARVMSDEFFSMC 20  
 Db 242 CHHHSRVARVMSDEFFSMC 261  
 RESULT 5  
 AAW06403  
 ID AAW06403 standard; protein; 315 AA.  
 XX  
 XX AAW06403;  
 XX  
 XX 25-FEB-1997 (first entry)  
 DT  
 XX Verotoxigenic E. coli toxin (VT1) subunit A.  
 XX  
 XX Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;  
 KW haemolytic uraemic syndrome; detection.  
 XX

OS Escherichia coli.  
 PN WO9630043-A1.  
 XX  
 XX 03-OCT-1996.  
 PD  
 XX 25-MAR-1996; 96WO-US004093.  
 PF  
 XX 24-MAR-1995; 95US-00410058.  
 PR  
 XX (OPHI-) OPHIDIAN PHARM INC.  
 PA  
 XX Carroll SB, Stafford DC, Padhye NV;  
 PI  
 XX WPI; 1996-505779/50.  
 XX  
 XX N-PSDB; AAT42649.  
 DR  
 XX Compn. contg. neutralising antitoxin against E.coli vero-toxin - used to  
 PT treat intoxicated individuals, and as a prophylactic against diarrhoeal  
 PT disease or extra-intestinal complications of E.coli infection.  
 XX  
 XX Example 6; Page 51; 101pp; English.  
 PS  
 XX Compositions containing neutralising antitoxin against one or more E.  
 CC coli verotoxin (VT) can be used to treat intoxicated adults and children  
 CC with enteric bacterial infections. They may also be used as prophylactics  
 CC e.g. as a vaccine, against diarrhoeal disease or the development of extra  
 CC -intestinal complications of E.coli infection, especially haemolytic  
 CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in  
 CC a sample. The VT is recombinant, preferably a fusion protein containing a  
 CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence  
 XX  
 XX Sequence 315 AA;  
 Query Match 100.0%; Score 114; DB 2; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0;  
 Qy 1 CHHHSRVARVMSDEFFSMC 20  
 Db 264 CHHHSRVARVMSDEFFSMC 283  
 RESULT 6  
 AAW21702  
 ID AAW21702 standard; protein; 315 AA.  
 XX  
 XX AAW21702;  
 AC  
 XX  
 XX 17-OCT-2003 (revised)  
 DT  
 XX 25-MAR-2003 (revised)  
 DT  
 XX 26-SEP-1997 (first entry)  
 DT  
 XX Shiga-like toxin (SLT-1) RIP.  
 XX  
 XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;  
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;  
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat;  
 KW ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.  
 XX  
 XX Bacteriophage H-19B.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH 145..155  
 FT Region /note= "Position of possible insertion of internal  
 FT peptide linker sequence"  
 FT  
 XX US5635384-A.  
 PN  
 XX 03-JUN-1997.  
 PD  
 XX 26-JAN-1995; 95US-00378761.  
 XX  
 XX

PR 11-JUN-1990; 90US-00535636.  
 PR 09-DEC-1992; 92US-00987927.  
 XX PA (DOWC ) DOWELANCO.  
 XX PI Hey TD, Morgan AER, Walsh TA;  
 XX DR WPI; 1997-309831/28.  
 XX DR WPI; 1997-309831/28.  
 XX PT Inactive precursor of maize ribosome-inactivating protein - also chimeric  
 PT ribosome-inactivating protein precursors containing internal linker  
 PT sequences.  
 XX PS Claim 2; Col 113-116; 121pp; English.  
 XX CC The sequences given in AAW21698-710 represent Ribosome Inactivating  
 CC Proteins (RIP's), which may be used in the construction of the proRIP of  
 CC the invention. The proRIP has a selectively removable, internal peptide  
 CC linker. The precursor sequence is incapable of inactivating eukaryotic  
 CC ribosomes, but can be converted by removal of the linker into a protein  
 CC having alpha and beta fragments and being capable of inactivating  
 CC eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein  
 CC synthesis. They possess a highly specific N-glycosidase activity which  
 CC cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S  
 CC RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. make  
 CC cancer cells and HIV-infected T cells. The inactive proRIP proteins make  
 CC it possible to provide protein synthesis inhibitors with uses in  
 CC practical and improved ways not before possible. The RIP can be used to  
 CC make cytotoxic conjugates. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 XX SQ Sequence 315 AA;  
 Query Match 100.0%; Score 114; DB 2; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHHHSRVARMSDEFFPSMC 20  
 DB 264 CHHHSRVARMSDEFFPSMC 283  
 RESULT 7  
 AAW25139  
 ID AAW25139 standard; protein; 315 AA.  
 XX AC AAW25139;  
 XX AC AAW25139;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 02-DEC-1997 (first entry)  
 XX DE SLT-1 (a ribosome inhibitory protein) inactive precursor.  
 XX KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;  
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;  
 KW Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin A; MAP;  
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;  
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;  
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome.  
 XX OS Synthetic.  
 XX FN US5646026-A.  
 XX PD 08-JUL-1997.  
 XX XX 07-JUN-1995; 95US-00485286.  
 XX PR 11-JUN-1990; 90US-00535636.  
 PR 09-DEC-1992; 92US-00987927.  
 PR 26-JAN-1995; 95US-00378761.  
 XX

PA (DOWC ) DOWELANCO.  
 XX Hey TD, Morgan AER, Walsh TA;  
 XX DR WPI; 1997-362934/33.  
 XX DR DNA encoding pro-ribosome inactivating proteins - inactive precursors of  
 PT ribosome inactivating proteins; can be expressed in eukaryotic cells  
 PT without causing cell death.  
 XX PS Claim 4; Col 115-116; 186pp; English.  
 XX CC AAW25139 represents an SLT-1 (a ribosome inhibitory protein, RIP) protein  
 CC which was engineered to contain a selectively removable internal peptide  
 CC linker sequence separating the alpha and beta units of the RIP. When  
 CC separated the two units regain activity and are capable of inactivating  
 CC eukaryotic ribosomes and hence preventing protein production. Many  
 CC different RIPs may be produced with an internal linker including maize  
 CC RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and Saporin. The RIPs  
 CC can be used in the construction of therapeutic toxins targeted to  
 CC specific cells such as tumour cells via the attachment of a targeting  
 CC polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy  
 CC (see US4869903). There is interest in expressing RIP recombinantly in  
 CC host eukaryotic cells, because of the capacity to provide correct post-  
 CC translational processing. However, RIPs effectively inhibit protein  
 CC synthesis in eukaryotic cells resulting in cell death. Since the inactive  
 CC RIP proteins are not cytotoxic to eukaryotic cells, they can be  
 CC recombinantly expressed in such cells and then converted to active RIP  
 CC proteins. (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 315 AA;  
 Query Match 100.0%; Score 114; DB 2; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CHHHSRVARMSDEFFPSMC 20  
 DB 264 CHHHSRVARMSDEFFPSMC 283  
 RESULT 8  
 AAY96681  
 ID AAY96681 standard; protein; 315 AA.  
 XX AC AAY96681;  
 XX AC AAY96681;  
 XX DT 26-SEP-2000 (first entry)  
 XX DE E. coli verotoxin 1 subunit A.  
 XX KW VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;  
 KW recombinant production; screening; dairy; anti-bacterial; vaccine.  
 OS Escherichia coli.  
 XX FN US6080400-A.  
 XX PD 27-JUN-2000.  
 XX PF 13-MAR-1997; 97US-00816977.  
 XX PR 24-MAR-1995; 95US-00410058.  
 XX PA (OPHI-) OPHIDIAN PHARM INC.  
 XX PI Williams JA, Byrne LM;  
 XX DR WPI; 2000-451195/39.  
 DR N-PSDB; AAAS1194.  
 XX PT Bacterial cell for recombinantly expressing bacterial toxins in large  
 PT quantities useful for immunization and treatment of bacterial infections,

PT comprises expression vector encoding bacterial toxin.  
 PS Example 6; Col 69-71; 83pp; English.  
 XX

CC The invention relates to antitoxin therapy for humans and other animals.  
 CC Antitoxins which neutralize the pathologic effects of *Escherichia coli*  
 CC toxins are generated by immunization of avian hosts with recombinant  
 CC toxin fragments. The recombinant *E. coli* verotoxin (VT) is a fusion  
 CC protein comprising a non-verotoxin protein (especially an affinity tag)  
 CC fused to a portion of the VT-1 or VT-2 sequence. The VT B chains are  
 CC small proteins (approximately 8 kDa), so use of a small affinity tag was  
 CC preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates  
 CC single step affinity purification of subunits from periplasmic extracts.  
 CC However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains,  
 CC expression of maltose binding protein (MBP) fused subunits was  
 CC undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced  
 CC promoter control is necessary to permit cell viability. Bacterial host  
 CC cells expressing a recombinant expression vector encoding a polyhistidine  
 CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is  
 CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"  
 CC indicates that the vector encodes the preprotein form of the protein and  
 CC "L-" indicates that the vector encodes the mature form of the protein.  
 CC The bacterial cell is capable of expressing large quantities (40 mg/l) of  
 CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting  
 CC bacterial toxins in environmental samples including soil, water,  
 CC industrial samples, biological samples and samples obtained from food and  
 CC dairy processing instruments  
 XX Sequence 315 AA;  
 SQ

Query Match 100.0%; Score 114; DB 3; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFPSSMC 20  
 |||||  
 DB 264 CHHHSRVARMSDEFPSSMC 283

RESULT 9  
 AAU77817  
 ID AAU77817 standard; protein; 315 AA.  
 AC  
 AC AAU77817;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE *E. coli* verotoxin VT1-A chain protein.  
 XX  
 KW Verotoxin; VT1-A; antitoxin; antidiarrheal; antibacterial; haemostatic;  
 KW vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome;  
 KW thrombotic thrombocytopenic purpura.  
 XX  
 OS *Escherichia coli*.  
 XX  
 PN US2002012658-A1.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 16-JUN-1999; 99US-00334477.  
 XX  
 PR 13-MAR-1997; 97US-00816977.  
 XX  
 PA (WILL/) WILLIAMS J A.  
 PA (BYRN/) BYRNE L M.  
 PA (PUGH/) PUGH C S G.  
 XX  
 PI Williams JA, Byrne LM, Pugh CSG;  
 XX  
 DR WPI; 2002-205094/26.  
 DR N-PSDB; ABK11775.  
 XX  
 PT New recombinant expression vector encoding affinity tag and *Escherichia*

PT coli type 1 or type 2 verotoxin, useful for treating or preventing  
 PT diseases due to *E. coli* verotoxins and in producing vaccines.  
 XX  
 PS Example 6; Page 38-39; 98pp; English.  
 XX

CC This invention relates to a recombinant expression vector encoding an  
 CC affinity tag and protein comprising at least a portion of a bacterial  
 CC toxin consisting of *Escherichia coli* type 1 or type 2 verotoxin. The  
 CC expression vector can be used to produce recombinant verotoxin protein  
 CC which can be used to create a vaccine against diseases caused by *E. coli*  
 CC such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins  
 CC are useful for treating humans and animals intoxicated with a bacterial  
 CC toxin, particularly *E. coli* verotoxin. The antitoxins may also be used in  
 CC the preventative treatment and in diagnostic assays to detect the  
 CC presence of a toxin in a sample. The polypeptides derived from *E. coli*  
 CC verotoxins are useful as immunogens for the production of vaccines.  
 CC including multivalent vaccines and antitoxins, which can be administered  
 CC to a subject at risk of diarrhoeal disease or at risk of developing extra  
 CC -intestinal complications of *E. coli* infections, e.g. haemolytic uremic  
 CC syndrome, thrombotic thrombocytopenic purpura. The present sequence  
 CC represents the *E. coli* verotoxin protein VT1-A used to create the  
 CC expression vectors of the invention  
 XX Sequence 315 AA;  
 SQ

Query Match 100.0%; Score 114; DB 5; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFPSSMC 20  
 |||||  
 DB 264 CHHHSRVARMSDEFPSSMC 283

RESULT 10  
 ADC00545  
 ID ADC00545 standard; protein; 315 AA.  
 XX  
 AC ADC00545;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Enterohaemorrhagic *E. coli* O157:H7-specific protein SEQ ID NO: 590.  
 XX  
 KW enterohaemorrhagic; anti-bacterial.  
 XX  
 OS *Escherichia coli*; O157:H7.  
 XX  
 PN JP2002355074-A.  
 XX  
 PD 10-DEC-2002.  
 XX  
 PF 24-JAN-2002; 2002JP-00015959.  
 XX  
 PR 24-JAN-2001; 2001JP-00112010.  
 XX  
 PA (UYTS-) UNIV TSUKUBA.  
 XX  
 DR WPI; 2003-451640/43.  
 XX  
 PT Enterohaemorrhagic *Escherichia coli* O157:H7-specific nucleic acid molecule  
 PT and a polypeptide and its use, a polypeptide, a vector and a host cell.  
 XX  
 PS Claim 3; SEQ ID NO 590; 2067pp; Japanese.  
 XX  
 CC The invention relates to a novel enterohaemorrhagic *Escherichia coli*  
 CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention  
 CC has anti-bacterial activity. The polypeptide can be used in detection  
 CC and/or treatment of O157:H7 infection. The nucleotide sequence of the  
 CC genome of Enterohaemorrhagic *E. coli* O157:H7 was determined. The present  
 CC sequence represents an *E. coli* O157:H7-specific polypeptide of the  
 CC invention.  
 XX

```

SQ Sequence 315 AA;
Query Match 100.0%; Score 114; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFFPSMC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 CHHHSRVARWASDEFFPSMC 283

RESULT 11
ADH34319
ID ADH34319 standard; protein; 315 AA.
XX
AC ADH34319;
XX
DT 11-MAR-2004 (first entry)
XX
DE Verotoxin 1 (VT1) A subunit.
XX
XX Attenuated verotoxin; attenuated VT; mutant A subunit; troponin I;
KW fusion protein; cancer; cytostatic; verotoxin 1; VT1; A subunit.
XX
XX Escherichia coli; O157:H7.
XX
XX WO2003066854-A1.
XX
XX 14-AUG-2003.
XX
XX 03-FEB-2003; 2003WO-JP001043.
XX
XX 04-FEB-2002; 2002JP-00026577.
XX
XX (YOSH/) YOSHIDA H.
XX
XX Yoshida H, Liu X;
XX
XX WPI; 2003-646309/61.
XX
XX Attenuated verotoxin controls tumor growth for treatment of cancer.
XX
XX Disclosure; Fig 3; 56pp; Japanese.
XX
XX The invention relates to attenuated verotoxins (VTs) comprising mutations
CC in one or more of the regions spanning residues 167-172 or 202-207 of the
CC mature verotoxin A subunit. The invention also relates to the mutant
CC verotoxin A subunit and the DNA encoding it; anticancer agents containing
CC the novel mutant A subunit; a fusion protein comprising the mutant
CC verotoxin A subunit and a ligand, especially troponin I, which binds to a
CC cancer cell; a fusion gene encoding the mutant A subunit/troponin I
CC fusion protein; and vectors encoding either the mutant verotoxin A
CC subunit, or the fusion gene of the invention. The attenuated verotoxins,
CC A subunits, fusion proteins, and polynucleotides encoding them are useful
CC in the treatment of cancer. The present sequence represents the A subunit
CC of verotoxin 1 (VT1).
XX
SQ Sequence 315 AA;
Query Match 100.0%; Score 114; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFFPSMC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 CHHHSRVARWASDEFFPSMC 283

RESULT 12
AAW25786
ID AAW25786 standard; protein; 316 AA.
XX
AC AAW25786;
XX

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XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1998 (first entry)
XX
DE Phage H19B shiga-like toxin.
XX
XX Shiga-like toxin; slt-A gene; hybrid protein; cell delivery;
KW cell binding ligand; translocation domain; diphtheria toxin B';
KW interleukin-2; T-cell lymphoma; organ rejection; therapy; ss.
XX
XX Bacteriophage H-19B.
XX
XX US5668255-A.
XX
XX 16-SEP-1997.
XX
XX 04-AUG-1993; 93US-00102387.
XX
XX 07-JUN-1984; 84US-00618199.
XX 25-APR-1985; 85US-00726808.
XX 07-JUN-1985; 85US-00742554.
XX 22-DEC-1989; 89US-00456095.
XX 14-JUN-1990; 90US-00538276.
XX 27-JUN-1991; 91US-00722484.
XX
XX (SERA-) SERAGEN INC.
XX
XX Murphy JR;
XX
XX WPI; 1997-470103/43.
XX N-PSDB; AAT91637.
XX
XX New hybrid molecules for delivery of agents to cells - comprise a binding
XX domain of a cell binding ligand and a portion of a trans-location domain
XX of a protein.
XX
XX Example 3; Fig 8A-C; 30pp; English.
XX
XX This protein comprises the Escherichia coli phage H19B Shiga-like toxin.
XX DNA (see AAT91637) encoding the A subunit of the Shiga-like toxin was
XX used to construct a Shiga-like toxin A-diphtheria toxin B'-interleukin-2
XX (SLTA-DTB'-IL2) gene that was expressed in E. coli. The hybrid protein
XX can be isolated and used to treat conditions involving over-production of
XX cells bearing IL2 receptors, such as certain i-cell lymphomas and organ
XX transplant rejection crises. The hybrid inactivates ribosomes in cells
XX bearing IL2 receptors, resulting in cessation of protein synthesis and
XX death of target cells. Claimed hybrid proteins comprise a translocation
XX domain and a cell binding domain from e.g. a hormone, growth factor or
XX protein toxin. The hybrid molecules can be used for the delivery of
XX agents (e.g. therapeutic genes, toxins, detectable labels) into cells.
XX The use of a translocation mechanism ensures that the hybrid will be
XX effective in relatively low doses, since a high proportion of the
XX subsequence of interest will be taken into the targeted cells. The hybrid
XX molecules can be manufactured as a single hybrid recombinant protein,
XX permitting reproducibility, consistency, and the precise control of
XX composition. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17
XX -OCT-2003 to standardise OS field)
XX
SQ Sequence 316 AA;
Query Match 100.0%; Score 114; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFFPSMC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 CHHHSRVARWASDEFFPSMC 283

RESULT 13
AAW06407
ID AAW06407 standard; protein; 323 AA.

```



```

XX AC AAW06407;
XX DT 25-FEB-1997 (first entry)
XX DE Histidine tagged verotoxinogenic E. coli toxin (VT1) subunit A.
XX KW Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;
XX KW haemolytic uraemic syndrome; detection.
XX OS Escherichia coli.
XX PN WO9630043-A1.
XX PD 03-OCT-1996.
XX PF 25-MAR-1996; 96WO-US004093.
XX PR 24-MAR-1995; 95US-00410058.
XX PA (OPHI-) OPHIDIAN PHARM INC.
XX PI Carroll SB, Stafford DC, Padhye NV;
XX DR WPI; 1996-505779/50.
XX DR N-PSDB; AAT42663.
XX PS Compn. contg. neutralising antitoxin against E.coli vero-toxin - used to
XX PT treat intoxicated individuals, and as a prophylactic against diarrhoeal
XX PT disease or extra-intestinal complications of E.coli infection.
XX PS Example 6; Page 61-62; 101pp; English.
XX CC Compositions containing neutralising antitoxin against one or more E.
XX CC coli verotoxin (VT) can be used to treat intoxicated adults and children
XX CC with enteric bacterial infections. They may also be used as prophylactics
XX CC e.g. as a vaccine, against diarrhoeal disease or the development of extra
XX CC -intestinal complications of E.coli infection, especially haemolytic
XX CC uraemic syndrome. The antitoxin can also be used to detect E. coli VT in
XX CC a sample. The VT is recombinant, preferably a fusion protein containing a
XX CC non-VT protein sequence and part of the E.coli VT1 or VT2 sequence. This
XX CC is a histidine tagged version of subunit A of VT1 as expressed from the
XX CC vector pET-23b
XX SQ Sequence 323 AA;
    Query Match 100.0%; Score 114; DB 2; Length 323;
    Best Local Similarity 100.0%; Pred. No. 1.2e-10;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHHHASRVARVASDEFFPSMC 20
DB 264 CHHHASRVARVASDEFFPSMC 283

RESULT 14
ID AAY96686
XX AAY96686 standard; protein; 323 AA.
XX AC AAY96686;
XX DT 26-SEP-2000 (first entry)
XX DE Recombinant E. coli VT-1 A-polyhistidine fusion protein.
XX KW VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
XX KW recombinant production; screening; dairy; anti-bacterial; vaccine;
XX KW polyhistidine.
XX OS Escherichia coli.
XX OS Synthetic.
XX OS Chimeric.

```

```

FH Key Location/Qualifiers
FT Protein 1..315
FT /label= Verotoxin-1_subunit_A
FT Peptide 316..323
FT /label= Polyhistidine_affinity_tag
XX US6080400-A.
XX 27-JUN-2000.
XX 13-MAR-1997; 97US-00816977.
XX 24-MAR-1995; 95US-00410058.
XX (OPHI-) OPHIDIAN PHARM INC.
XX Williams JA, Byrne LM;
XX WPI; 2000-451195/39.
XX DR N-PSDB; AAS51208.
XX PT Bacterial cell for recombinantly expressing bacterial toxins in large
XX PT quantities useful for immunization and treatment of bacterial infections,
XX PT comprises expression vector encoding bacterial toxin.
XX PS Example 6; Col 89-90; 83pp; English.
XX CC The invention relates to antitoxin therapy for humans and other animals.
XX CC Antitoxins which neutralize the pathologic effects of Escherichia coli
XX CC toxins are generated by immunization of avian hosts with recombinant
XX CC toxin fragments. The recombinant E. coli verotoxin (VT) is a fusion
XX CC protein comprising a non-verotoxin protein (especially an affinity tag)
XX CC fused to a portion of the VT-1 or VT-2 sequence. The VT B chains are
XX CC small proteins (approximately 8 kDa), so use of a small affinity tag was
XX CC preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates
XX CC single step affinity purification of subunits from periplasmic extracts.
XX CC However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains,
XX CC expression of maltose binding protein (MBP) fused subunits was
XX CC undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced
XX CC promoter control is necessary to permit cell viability. Bacterial host
XX CC cells expressing a recombinant expression vector encoding a polyhistidine
XX CC affinity tag and a portion of the VT-2 B chain are claimed. The vector is
XX CC chosen from pET24hisVT2BL+, pET24hisVT2BL- and pET24VT2B, where "L+"
XX CC "L-" indicates that the vector encodes the preprotein form of the protein and
XX CC "L-" indicates that the vector encodes the mature form of the protein.
XX CC The bacterial cell is capable of expressing large quantities (40 mg/l) of
XX CC VT-2B. The toxins are useful for immunizing non-mammals and for detecting
XX CC bacterial toxins in environmental samples including soil, water,
XX CC industrial samples, biological samples and samples obtained from food and
XX CC dairy processing instruments
XX SQ Sequence 323 AA;
    Query Match 100.0%; Score 114; DB 3; Length 323;
    Best Local Similarity 100.0%; Pred. No. 1.2e-10;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHHHASRVARVASDEFFPSMC 20
DB 264 CHHHASRVARVASDEFFPSMC 283

RESULT 15
ID AAU77822
XX AAU77822 standard; protein; 323 AA.
XX AC AAU77822;
XX DT 05-JUN-2002 (first entry)
XX DE HIS-tagged E. coli VT-1A verotoxin protein.
XX KW Verotoxin; VT1-A; antitoxin; antidiarrheal; antibacterial; haemostatic;

```

KW vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome;  
KW thrombotic thrombocytopenic purpura.

OS Escherichia coli.  
OS Synthetic.

XX Key Location/Qualifiers  
XX Peptide 316..323  
FT /note= "C terminal peptide with HIS tag"

XX US2002012658-A1.

XX 31-JAN-2002.

XX PF 16-JUN-1999; 99US-00334477.

XX PR 13-MAR-1997; 97US-00816977.

XX PA (WILL/) WILLIAMS J A.  
XX PA (BYRN/) BYRNE L M.  
XX PA (PUGH/) PUGH C S G.

XX PI Williams JA, Byrne LM, Pugh CSG;

XX DR WPI; 2002-205094/26.  
XX DR N-PSDB; ASK11789.

XX New recombinant expression vector encoding affinity tag and Escherichia  
PT coli type 1 or type 2 verotoxin, useful for treating or preventing  
PT diseases due to E. coli verotoxins and in producing vaccines.

XX PS Claim 1; Page 48-49; 98pp; English.

XX This invention relates to a recombinant expression vector encoding an  
CC affinity tag and protein comprising at least a portion of a bacterial  
CC toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The  
CC expression vector can be used to produce recombinant verotoxin protein  
CC which can be used to create a vaccine against diseases caused by E. coli  
CC such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins  
CC are useful for treating humans and animals intoxicated with a bacterial  
CC toxin, particularly E. coli verotoxin. The antitoxins may also be used in  
CC the preventative treatment and in diagnostic assays to detect the  
CC presence of a toxin in a sample. The polypeptides derived from E. coli  
CC verotoxins are useful as immunogens for the production of vaccines,  
CC including multivalent vaccines and antitoxins, which can be administered  
CC to a subject at risk of diarrhoeal disease or at risk of developing extra  
CC -intestinal complications of E. coli infections, e.g. haemolytic uremic  
CC syndrome, thrombotic thrombocytopenic purpura. The present sequence  
CC represents the HIS tagged E.coli VT1-A verotoxin protein of the invention

XX SQ Sequence 323 AA;

Query Match 100.0%; Score 114; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARMASDEFPSC 20  
Db ||||||||||||||||  
264 CHHHSRVARMASDEFPSC 283

Search completed: February 10, 2006, 10:05:01  
Job time : 12.8856 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:05:19 ; Search time 2.73063 Seconds  
(without alignments)  
704.723 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARMSDEFFSMC 20

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	315	1	Shigella toxin cha
2	114	100.0	315	1	Shiga-like toxin c
3	114	100.0	315	2	Shiga-like toxin I
4	114	100.0	315	2	Shiga toxin I subu
5	114	100.0	315	2	Shiga toxin I subu
6	114	100.0	315	2	Shiga-like toxin I
7	50.5	44.3	365	2	hypothetical prote
8	50	43.9	451	2	hypothetical prote
9	49	43.0	2152	2	hypothetical prote
10	47	41.2	135	2	cell adhesion prot
11	47	41.2	252	2	conserved hypotet
12	46	40.4	196	2	probable transcrip
13	46	40.4	319	2	Shiga-like cytotox
14	46	40.4	507	2	pyridoxine 4-oxida
15	45	39.5	254	2	hypothetical prote
16	45	39.5	278	2	hypothetical prote
17	45	39.5	466	2	nicotinic acetylch
18	44	38.6	252	2	probable DNA-bind
19	44	38.6	308	2	D-ribose-binding p
20	44	38.6	318	2	Shiga-like toxin I
21	44	38.6	319	2	variant shiga-like
22	44	38.6	319	2	shiga-like toxin I
23	44	38.6	319	2	Shiga-like toxin I
24	44	38.6	319	2	hypothetical prote
25	44	38.6	319	2	Shiga toxin 2 subu
26	44	38.6	319	2	Shiga toxin 2 subu
27	44	38.6	319	2	shiga-like toxin I
28	44	38.6	319	2	verocytotoxin A ch
29	44	38.6	320	2	shiga-like toxin -

30 44 38.6 433 2 T04594 aldehyde dehydroge  
31 44 38.6 475 2 S45116 natriuretic peptid  
32 44 38.6 535 2 A54155 natriuretic peptid  
33 43 37.7 536 2 S71332 natriuretic peptid  
34 43 37.7 540 1 OYHUCR natriuretic peptid  
35 43 37.7 1149 2 T20891 hypothetical prote  
36 43 37.7 2437 2 S53611 MIBP1 protein - ra  
37 43 37.7 2500 1 WHHUE2 HIV-EP2 enhancer-b  
38 42 36.8 161 2 S76282 hypothetical prote  
39 42 36.8 285 2 B82842 spermidine synthas  
40 42 36.8 381 2 S58663 isocitrate dehydro  
41 42 36.8 387 2 T13147 isocitrate dehydro  
42 42 36.8 398 2 AD2944 fosmidomycin resis  
43 42 36.8 398 2 F98338 fosmidomycin resis  
44 42 36.8 404 2 AB0376 probable membrane  
45 42 36.8 406 1 JC5041 fosmidomycin resis

#### ALIGNMENTS

##### RESULT 1

A28626

Shigella toxin chain A precursor - Shigella dysenteriae

N;Alternate names: shiga toxin chain A

N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Shigella dysenteriae

C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004

C;Accession: A28626; S04021

R;Strockbine, N.A.; Jackson, M.P.; Sung, L.M.; Holmes, R.K.; O'Brien, A.D.

J. Bacteriol. 170, 1116-1122, 1988

A;Title: Cloning and sequencing of the genes for Shiga toxin from Shigella dysenteriae

A;Reference number: A91864; MUID:88139166; PMID:2830229

A;Contents: Type 1 3818T

A;Accession: A28626

A;Molecule type: DNA

A;Residues: 1-315 <STR>

A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI00000000DA9; GB:M19437; NID:G152784; PIDN:

R;Kozlov, Y.V.; Kabishev, A.A.; Fedchenko, V.I.; Baev, A.A.

Dokl. Biochem. 295, 216-220, 1987

A;Title: Cloning and primary structure of Shigella toxin genes.

A;Reference number: S04021

A;Accession: S04021

A;Molecule type: DNA

A;Residues: 1-315 <KOZ>

A;Cross-references: UNIPARC:UPI00000000DA9; EMBL:X07903; NID:G46946

C;Genetics:

A;Gene: stxA

C;Complex: heterohexamer of one A chain and five B chains (see PIR:XVEBBD)

C;Function:

A;Description: hydrolyzes the N-glycosidic bond of a specific adenine in 28S rRNA

C;Superfamily: Shigella toxin chain A

C;Keywords: cytotoxin; glycosidase; hexamer; hydrolase; RNA binding

F;1-22/Domain: signal sequence #status predicted <Sig>

F;23-315/Product: Shigella toxin chain A #status predicted <MAT>

Query Match 100.0%; Score 114; DB 1; Length 315;

Best Local Similarity 100.0%; Pred. No. 8e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CHHHSRVARMSDEFFSMC 20

|||||

Db 264 CHHHSRVARMSDEFFSMC 283

##### RESULT 2

XUBPH9

Shiga-like toxin chain A precursor - phage H19B

C;Species: phage H19B

A;Note: host Escherichia coli

C;Date: 30-Sep-1990 #sequence\_revision 30-Sep-1990 #text\_change 09-Jul-2004

C;Accession: A27052

R;Calderwood, S.B.; Auclair, F.; Donohue-Rolfe, A.; Keusch, G.T.; Mekalanos, J.J.

```

Proc. Natl. Acad. Sci. U.S.A. 84, 4364-4368, 1987
A;Title: Nucleotide sequence of the Shiga-like toxin genes of Escherichia coli.
A;Reference number: A27052; MUID:87260808; PMID:3299365
A;Accession: A27052
A;Molecule type: DNA
A;Residues: 1-315 <CAL>
A;Cross-references: UNIPROT:P08026; UNIPARC:UPI000000043F; GB:M16625; NID:g215043; PIDN:
C;Genetics:
A;Gene: sltA
C;Superfamily: Shigella toxin chain A
C;Keywords: toxin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-315/Product: Shiga-like toxin chain A #status predicted <MAT>

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 3
UN0725
Shiga-like toxin I chain A precursor [validated] - Escherichia coli
C;Species: Escherichia coli
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: UN0732; I68041; I68043; A61473; S47254; S47256; S47258
R;Paton, A.W.; Paton, J.C.; Goldwater, P.N.; Heuzenroeder, M.W.; Manning, P.A.
Gene 129, 87-92, 1993
A;Title: Sequence of a variant Shiga-like toxin type-I operon of Escherichia coli O111:H
A;Reference number: UN0725; MUID:93328129; PMID:8335264
A;Accession: UN0725
A;Molecule type: DNA
A;Residues: 1-315 <PAT>
A;Cross-references: UNIPROT:Q47647; UNIPARC:UPI000000BC490; GB:L04539; NID:gl47832; PIDN:
A;Experimental source: serotype O111:H(-)
R;Paton, A.W.; Beutin, L.; Paton, J.C.
Gene 153, 71-74, 1995
A;Title: Heterogeneity of the amino-acid sequences of Escherichia coli Shiga-like toxin
A;Reference number: I53932; MUID:95189106; PMID:7883188
A;Accession: I53932
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-170,'S',172-248,'E',250-315 <PAT1>
A;Cross-references: UNIPARC:UPI000000BA3CB; EMBL:Z36899; NID:g534987; PIDN:CAA85366.1; PI
A;Experimental source: serotype O48:H21
A;Note: submitted to the EMBL Data Library, August 1994
A;Accession: I68041
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-131,'S',133-170,'S',172-315 <PAT2>
A;Cross-references: UNIPARC:UPI000000B9ECB; EMBL:Z36900; NID:g535054; PIDN:CAA85368.1; PI
A;Experimental source: serotype O111:H(-)
A;Note: submitted to the EMBL Data Library, August 1994
A;Accession: I68043
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-170,'S',172-250,'V',252-273,'IVPN',278-284,'V',286-308,'I',310-311,'A',313
A;Cross-references: UNIPARC:UPI000000SD32; EMBL:Z36901; NID:g535088; PIDN:CAA85370.1; PI
R;Takao, T.; Tanabe, T.; Hong, Y.M.; Shimonishi, Y.; Kurazono, H.; Yutsudo, T.; Sasakawa
Microb. Pathog. 5, 357-369, 1988
A;Title: Identity of molecular structure of Shiga-like toxin I (VT1) from Escherichia co
A;Reference number: A61473
A;Accession: C61473
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170,'S',172-315 <PAT1>
A;Cross-references: UNIPARC:UPI0000000DA9
A;Experimental source: strain O157:H7
A;Accession: A61473

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```

A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-51;62-76;107-132,'XX',135-136;183-192;202-224,'XX',227-241;276-282,291-29
A;Cross-references: UNIPARC:UPI00001766F7; UNIPARC:UPI00001766F8; UNIPARC:UPI00001766F9;
A;Experimental source: strain O157:H7
C;Genetics:
A;Gene: SLT-1A
C;Superfamily: Shigella toxin chain A
C;Keywords: disulfide bond; toxin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-315/Product: Shiga-like toxin I chain A #status experimental <MAT>

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 4
F91000
Shiga toxin I subunit A precursor [imported] - Escherichia coli (strain O157:H7, substra
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91000
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <HAY>
A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI0000000DA9; GB:BA0000007; PIDN:BA836397.1;
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECa2974
C;Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20
Db 264 CHHHSRVARWASDEFFSMC 283

RESULT 5
H85845
Shiga toxin I subunit A precursor [imported] - Escherichia coli (strain O157:H7, substra
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85845
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85845
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Cross-references: UNIPROT:Q8X696; UNIPARC:UPI0000000DA9; GB:AE005174; NID:g12516395; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: stx1A
C;Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;

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Best Local Similarity 100.0%; Pred. No. 8e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFFPSMC 20  
Db 264 CHHHSRVARVASDEFFPSMC 283

RESULT 6  
A53887  
Shiga-like toxin I A chain precursor - page 933J  
C:Species: phase 933J  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: A53887  
R:Jackson, M.P.; Newland, J.W.; Holmes, R.K.; O'Brien, A.D.  
Microb. Pathog. 2, 147-153, 1987  
A:Title: Nucleotide sequence analysis of the structural genes for Shiga-like toxin I and II  
A:Reference number: A53887; MUID:89180929; PMID:3333796  
A:Accession: A53887  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-315 <JAC>  
A:Cross-references: UNIPROT:P08026; UNIPARC:UPI000000043F; GB:M19473; NID:g215072; PIDN:  
C:Superfamily: Shigella toxin chain A

Query Match 100.0%; Score 114; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 8e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFFPSMC 20  
Db 264 CHHHSRVARVASDEFFPSMC 283

RESULT 7  
T08577  
hypothetical protein T22P8.190 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T08577  
R:Bayan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16442  
A:Accession: T08577  
A:Molecule type: DNA  
A:Residues: 1-365 <BEV>  
A:Cross-references: UNIPROT:Q9T035; UNIPARC:UPI000000A6AFC; EMBL:AL050351; GSPDB:GN000062;  
A:Experimental source: cultivar Columbia; BAC clone T22P8  
C:Genetics:  
A:Gene: ATSP:T22P8.190  
A:Map position: 4  
C:Superfamily: conserved hypothetical protein containing F-box and Kelch domains

Query Match 44.3%; Score 50.5; DB 2; Length 365;  
Best Local Similarity 47.8%; Pred. No. 1.9;  
Matches 11; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 CHHHSRVA---RVASDEFFPSMC 20  
Db 140 CRSHTWREAPSMRVARDFFPSTC 162

RESULT 8  
T33763  
hypothetical protein Y55H10A.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T33763  
R:Antoniou, B.; Smith, A.; Gibson, A.  
submitted to the EMBL Data Library, October 1998  
A:Description: The sequence of C. elegans cosmid Y55H10A.  
A:Reference number: Z21402  
A:Accession: T33763

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-451 <ANT>  
A:Cross-references: UNIPROT:Q9TWT1; UNIPARC:UPI000007570D; EMBL:AF100675; PIDN:AAC69004.  
A:Experimental source: strain Bristol N2; clone Y55H10A  
C:Genetics:  
A:Gene: CRSP:Y55H10A.1  
A:Map position: 4  
A:Introns: 29/2; 57/1; 95/3; 233/1; 319/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein Y55H10A.1

Query Match 43.9%; Score 50; DB 2; Length 451;  
Best Local Similarity 58.8%; Pred. No. 2.8;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHHSRVARVASDEFFPS 18  
Db 151 HXKSRVRVATDEFNS 167

RESULT 9  
T45583  
hypothetical protein F11C1.210 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T45583  
R:Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: Z23007  
A:Accession: T45583  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2152 <BAR>  
A:Cross-references: UNIPROT:Q9SND1; UNIPARC:UPI000009D156; EMBL:AL132976  
A:Experimental source: cultivar Columbia; BAC clone F11C1  
C:Genetics:  
A:Map position: 3  
A:Introns: 53/3; 411/2; 1479/3; 1543/2; 1592/3; 1659/1; 1750/1; 1965/3  
A:Note: F11C1.210

Query Match 43.0%; Score 49; DB 2; Length 2152;  
Best Local Similarity 41.2%; Pred. No. 20;  
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 HHHSRVARVASDEFFPSM 19  
Db 131 HHVKVATLRGDEFPPL 147

RESULT 10  
A34653  
cell adhesion protein SOM1 - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 09-Jul-2004  
C:Accession: A34653  
R:Wong, Y.C.; Tsao, S.W.; Kakefuda, M.; Bernal, S.D.  
Biochem. Biophys. Res. Commun. 166, 984-992, 1990  
A:Title: cDNA cloning of a novel cell adhesion protein expressed in human squamous carci  
A:Reference number: A34653; MUID:90147818; PMID:2302251  
A:Accession: A34653  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <WON>  
A:Cross-references: UNIPROT:P17568; UNIPARC:UPI000014AAD6; GB:M33374; NID:g180232; PIDN:  
C:Keywords: cell adhesion

Query Match 41.2%; Score 47; DB 2; Length 135;  
Best Local Similarity 44.4%; Pred. No. 2.5;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVASDEFFPS 18  
Db 58 CAHHLIRLLKCRDPSFP 75

## RESULT 11

D95853  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: D95853  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: D95853  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-252 <KUR>  
A;Cross-references: UNIPROT:Q92X70; UNIPARC:UPI00000CB3EA; GB:AL591985; PIDN:CAC48492.1;  
A;Experimental source: strain 1021, megaplasmid pSymB  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: Smb20092  
A;Genome: plasmid

Query Match 41.2%; Score 47; DB 2; Length 252;

Best Local Similarity 52.9%; Pred. No. 4.7;

Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

## Qy 1 CHHHSRVARVASDEFP 17

Db 224 CRVHGSLRASDHLP 240

## RESULT 12

D83279  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: D83279  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: D83279  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-196 <STO>  
A;Cross-references: UNIPROT:Q9H2R6; UNIPARC:UPI00000CS58E; GB:AE004719; GB:AE004091; NID  
C;Genetics:  
A;Experimental source: strain PA01  
A;Gene: PA2931

Query Match 40.4%; Score 46; DB 2; Length 196;

Best Local Similarity 69.2%; Pred. No. 5.3;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

## Qy 8 VARMSDFPSMC 20

Db 95 VARFCSDFPRGC 107

## RESULT 13

I60446  
C;Species: Escherichia coli  
C;Title: Shiga-like cytotoxin subunit A - Escherichia coli

N;Alternate names: shiga-like toxin II variant chain A

C;Species: Escherichia coli

C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004

C;Accession: I60446; I57048; S31420

R;Paton, A.W.; Paton, J.C.; Heuzenroeder, M.W.; Goldwater, P.N.; Manning, P.A.

Microb. Pathog. 13, 225-236, 1992

A;Title: Cloning and nucleotide sequence of a variant Shiga-like toxin II gene from Eschi

A;Reference number: I60446; MUID:93180660; PMID:1291844

A;Accession: I60446

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-319 <RES>

A;Cross-references: UNIPROT:Q03037; UNIPARC:UPI00000BEE9B; EMBL:X65949; NID:G49089; PIDN:

R;Paton, A.W.; Paton, J.C.; Manning, P.A.

Microb. Pathog. 15, 77-82, 1993

A;Title: Polymerase chain reaction amplification, cloning and sequencing of variant Eschi

A;Reference number: I57048; MUID:94018566; PMID:8412629

A;Accession: I57048

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-197; 'G', 199-319 <RE2>

A;Cross-references: UNIPARC:UPI000016F4EF; GB:L11078; NID:G304950; PIDN:AAA16360.1; PID:

C;Superfamily: Shigella toxin chain A

C;Keywords: cytotoxin

Query Match 40.4%; Score 46; DB 2; Length 319;

Best Local Similarity 35.0%; Pred. No. 8.7;

Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

## Qy 1 CHHHSRVARVASDEFPSC 20

Db 263 CHHGARSVRANEEIQPEC 282

## RESULT 14

JY7855

Pyridoxine 4-oxidase (EC 1.1.3.12) - Microbacterium luteolum YK-1

N;Alternate names: PN 4-oxidase; pyridoxin 4-oxidase

C;Species: Microbacterium luteolum YK-1

C;Date: 18-Nov-2002 #sequence\_revision 18-Nov-2002 #text\_change 05-Oct-2004

C;Accession: JC7855; PC7192

R;Kaneda, Y.; Ohnishi, K.; Yagi, T.

Biosci. Biotechnol. Biochem. 66, 1022-1031, 2002

A;Title: Purification, Molecular cloning, and characterization of pyridoxine 4-oxidase f

A;Reference number: JC7855; MUID:22087109; PMID:12092811

A;Accession: JC7855

A;Molecule type: DNA

A;Residues: 1-507 <KAN>

A;Cross-references: UNIPARC:UPI000017CE48; DDBJ:AB049341

A;Experimental source: strain YK-1

A;Accession: PC7192

A;Molecule type: protein

A;Residues: 2-20;348-364 <KA2>

A;Cross-references: UNIPARC:UPI000017CE49; UNIPARC:UPI000017CE4A

C;Comment: This enzyme that is an FAD-dependent enzyme and a monomeric protein belongs t

ors to form pyridoxal and hydrogen peroxide or reduced forms of the acceptors. This enzy

C;Genetics:

A;Gene: pno

C;Superfamily: alcohol oxidase

C;Keywords: oxidoreductase

Query Match 40.4%; Score 46; DB 2; Length 507;

Best Local Similarity 57.1%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

## Qy 2 HHHSRVARVASDE 15

Db 446 HHHSRVARVASDE 459

## RESULT 15

S72759  
hypothetical protein B1496\_C2\_188 - Mycobacterium leprae

C;Species: Mycobacterium leprae  
 C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C;Accession: S72759; T11014  
 R;Smith, D.R.; Robison, K.  
 submitted to the EMBL Data Library, November 1993  
 A;Description: Mycobacterium leprae cosmid B1496.  
 A;Reference number: S72695  
 A;Accession: S72759  
 A;Molecule type: DNA  
 A;Residues: 1-254 <SMI>  
 A;Cross-references: UNIPROT:Q49688; UNIPARC:UPI00000D433C; EMBL:U00013; NID:g466868; PID  
 R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, September 1997  
 A;Reference number: Z16918  
 A;Accession: T11014  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-254 <PAR>  
 A;Cross-references: UNIPARC:UPI00000D433C; EMBL:Z99125; NID:g2398683; PIDN:CAB16173.1; E  
 C;Genetics:  
 A;Gene: MLC1536.29c  
 A;Start codon: GTG

Query Match 39.5%; Score 45; DB 2; Length 254;  
 Best Local Similarity 45.5%; Pred. No. 10;  
 Matches 10; Conservative 2; Mismatches 4; Indels 6; Gaps 2;  
 QY 1 CHHH--ASRVARMASDEFFSMC 20  
 ||| ||| :||| :  
 Db 196 QHHCPSVSHA----EEFPELC 213

Search completed: February 10, 2006, 10:14:04  
 Job time : 3.73063 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 16.9004 Seconds  
(without alignments)  
834.927 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARNASDEFFSMC 20

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	222	2	Q5ZPW9 ECOLI
2	114	100.0	236	2	Q5ZPX0 ECOLIC
3	114	100.0	237	2	Q5ZPX1 ECOLIC
4	114	100.0	240	2	Q5ZPX2 ECOLIC
5	114	100.0	242	2	Q5ZPX4 ECOLIC
6	114	100.0	243	2	Q5ZPX3 ECOLIC
7	114	100.0	243	2	Q5ZPX5 ECOLIC
8	114	100.0	248	2	Q5ZPX6 ECOLIC
9	114	100.0	254	2	Q5ZPX8 ECOLIC
10	114	100.0	259	2	Q5ZPX9 ECOLIC
11	114	100.0	276	2	Q5ZPY0 ECOLIC
12	114	100.0	313	2	Q5ZPY1 ECOLIC
13	114	100.0	315	1	Q5ZPY2 ECOLIC
14	114	100.0	315	1	SLTA_BPH10
15	114	100.0	315	2	Q5ZPW9 ECOLIC
16	114	100.0	315	2	Q5ZPW9 ECOLIC
17	114	100.0	315	2	Q5ZPW9 ECOLIC
18	114	100.0	315	2	Q5ZPW9 ECOLIC
19	114	100.0	315	2	Q5ZPW9 ECOLIC
20	114	100.0	315	2	Q5ZPW9 ECOLIC
21	114	100.0	315	2	Q5ZPW9 ECOLIC
22	114	100.0	315	2	Q5ZPW9 ECOLIC
23	114	100.0	315	2	Q5ZPW9 ECOLIC
24	114	100.0	315	2	Q5ZPW9 ECOLIC
25	114	100.0	315	2	Q5ZPW9 ECOLIC
26	114	100.0	315	2	Q5ZPW9 ECOLIC
27	114	100.0	315	2	Q5ZPW9 ECOLIC
28	114	100.0	315	2	Q5ZPW9 ECOLIC
29	114	100.0	315	2	Q5ZPW9 ECOLIC
30	114	100.0	315	2	Q5ZPW9 ECOLIC
31	114	100.0	315	2	Q5ZPW9 ECOLIC

32 114 100.0 315 2 Q77M7\_9CAUD Q77M7 phage phi 4  
33 105 92.1 315 2 Q83XK3 ECOLI Q83XK3 escherichia  
34 96 84.2 315 2 Q94M00\_9VIRU Q94M00 bacterioph  
35 96 84.2 315 2 Q47640 ECOLI Q47640 escherichia  
36 96 84.2 315 2 Q8V67 ECOLI Q8V67 escherichia  
37 90 78.9 315 2 Q8V64 ECOLI Q8V64 escherichia  
38 89 78.1 251 2 Q5ZPX7 ECOLI Q5ZPX7 escherichia  
39 86 75.4 315 2 Q8L168 ECOLI Q8L168 escherichia  
40 52 45.6 427 2 Q4UWU4\_XANCP Q4UWU4 xanthomonas  
41 52 45.6 427 2 Q8P7A8\_XANCP Q8P7A8 xanthomonas  
42 50.5 44.3 365 2 Q9T035\_ARATH Q9T035 arabidopsis  
43 50 43.9 373 2 Q4T41\_1TETNG Q4T41 tetradon n  
44 50 43.9 451 2 Q9T7W1\_CAENORHABDI Q9T7W1 caenorhabdi  
45 49 43.0 325 2 Q56W68\_ARATH Q56W68 arabidopsis

#### ALIGNMENTS

RESULT 1  
Q5ZPW9 ECOLI  
ID Q5ZPW9 ECOLI PRELIMINARY; PRT; 222 AA.  
AC Q5ZPW9;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Verocytotoxin 1 (Fragment).  
GN Name=VT1;  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC CATRAINE-372;  
RA Catraime T.M.;  
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ537526; CAD68999.1; -; Genomic\_DNA.  
DR SMR; Q5ZPW9: 1-222.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.  
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
FT NON TER 1 222  
FT NON TER 1 222  
SQ SEQUENCE 222 AA; 24698 MW; F29BF3CE24419E29 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARNASDEFFSMC 20  
|||||  
Db 196 CHHHSRVARNASDEFFSMC 215

RESULT 2  
Q5ZPX0 ECOLI  
ID Q5ZPX0 ECOLI PRELIMINARY; PRT; 236 AA.  
AC Q5ZPX0;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Verocytotoxin 1 (Fragment).  
GN Name=VT1;  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.

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OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=348;
RA "Rapid Diagnostic Methods for Food Borne Pathogens.";
RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ537525; CAD68998.1; -, Genomic_DNA.
DR SMR; Q5ZPX0; 1-236.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 236
FT NON_TER 236
SQ SEQUENCE 236 AA; 26045 MW; F8EEDF81890F04C0 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVMSDEFPSSMC 20
Db 207 CHHHSRVARVMSDEFPSSMC 226

RESULT 3
Q5ZPX1 ECOLI
ID Q5ZPX1 ECOLI PRELIMINARY; PRT; 237 AA.
AC Q5ZPX1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=333;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537524; CAD68997.1; -, Genomic_DNA.
DR SMR; Q5ZPX1; 1-237.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 237
FT NON_TER 237
SQ SEQUENCE 237 AA; 26182 MW; D578EEDF81890F04 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVMSDEFPSSMC 20
Db 207 CHHHSRVARVMSDEFPSSMC 226

RESULT 4
Q5ZPX4 ECOLI
ID Q5ZPX4 ECOLI PRELIMINARY; PRT; 242 AA.
AC Q5ZPX4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=354;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537521; CAD68994.1; -, Genomic_DNA.
DR SMR; Q5ZPX4; 1-242.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 242
FT NON_TER 242
SQ SEQUENCE 242 AA; 26615 MW; A32A72928BB03D43 CRC64;
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Q5ZPX2 ECOLI
ID Q5ZPX2 ECOLI PRELIMINARY; PRT; 240 AA.
AC Q5ZPX2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=359;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537523; CAD68996.1; -, Genomic_DNA.
DR SMR; Q5ZPX2; 1-240.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 240
FT NON_TER 240
SQ SEQUENCE 240 AA; 26538 MW; B46AA23578EDF81 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARVMSDEFPSSMC 20
Db 207 CHHHSRVARVMSDEFPSSMC 226
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RESULT 5
Q5ZPX4 ECOLI
ID Q5ZPX4 ECOLI PRELIMINARY; PRT; 242 AA.
AC Q5ZPX4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=354;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537521; CAD68994.1; -, Genomic_DNA.
DR SMR; Q5ZPX4; 1-242.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1
FT NON_TER 242
FT NON_TER 242
SQ SEQUENCE 242 AA; 26615 MW; A32A72928BB03D43 CRC64;
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Query Match 100.0%; Score 114; DB 2; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFPSSMC 20  
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 DB 216 CHHHSRVARWASDEFPSSMC 235

RESULT 6  
 Q5ZPX3\_ECOLI  
 ID Q5ZPX3\_ECOLI PRELIMINARY; PRT; 243 AA.  
 AC Q5ZPX3;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Verocytotoxin 1 (Fragment).  
 GN Name=Vtl;  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=352;  
 RA Catarame T.M.;  
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ537522; CAD68995.1; -; Genomic\_DNA.  
 DR SMR; Q5ZPX3; 1-243.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 FT NON TER 1  
 FT NON TER 243  
 SQ SEQUENCE 243 AA; 26765 MW; 1E58F46958FD9469 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFPSSMC 20  
 |||||  
 DB 209 CHHHSRVARWASDEFPSSMC 228

RESULT 7  
 Q5ZPX5\_ECOLI  
 ID Q5ZPX5\_ECOLI PRELIMINARY; PRT; 243 AA.  
 AC Q5ZPX5;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Verocytotoxin 1 (Fragment).  
 GN Name=Vtl;  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=381;  
 RA Catarame T.M.;  
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ537520; CAD68993.1; -; Genomic\_DNA.  
 DR SMR; Q5ZPX5; 1-243.

DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 FT NON TER 1  
 FT NON TER 243  
 SQ SEQUENCE 243 AA; 26617 MW; 4A69B4A3538DE250 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFPSSMC 20  
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 DB 218 CHHHSRVARWASDEFPSSMC 237

RESULT 8  
 Q5ZPX6\_ECOLI  
 ID Q5ZPX6\_ECOLI PRELIMINARY; PRT; 248 AA.  
 AC Q5ZPX6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Verocytotoxin 1 (Fragment).  
 GN Name=Vtl;  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CHI;  
 RA Catarame T.M.;  
 RT "Rapid Diagnostic Methods for Food Borne Pathogens.";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ537519; CAD68992.1; -; Genomic\_DNA.  
 DR SMR; Q5ZPX6; 4-248.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 FT NON TER 1  
 FT NON TER 248  
 SQ SEQUENCE 248 AA; 27189 MW; 653792826D462PED CRC64;

Query Match 100.0%; Score 114; DB 2; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHHSRVARWASDEFPSSMC 20  
 |||||  
 DB 222 CHHHSRVARWASDEFPSSMC 241

RESULT 9  
 Q5ZPX8\_ECOLI  
 ID Q5ZPX8\_ECOLI PRELIMINARY; PRT; 254 AA.  
 AC Q5ZPX8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Verocytotoxin 1 (Fragment).  
 GN Name=Vtl;  
 OS Escherichia coli.

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBi_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=361;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537517; CAD6899.1; -; Genomic_DNA.
DR SMR; Q52PX8; 1-254.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 254
FT NON_TER 254 254
SQ SEQUENCE 254 AA; 27842 MW; AC3BF7F69D9D1A52 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
| | | | | | | | | | | | | | | | | |
Db 228 CHHHSRVARMSDEFFPSMC 247

RESULT 10
Q52PX9_ECOLI
ID Q52PX9_ECOLI PRELIMINARY; PRT; 259 AA.
AC Q52PX9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBi_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=332;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for Food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537516; CAD6899.1; -; Genomic_DNA.
DR SMR; Q52PX9; 15-259.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 259
FT NON_TER 259 259
SQ SEQUENCE 259 AA; 28482 MW; 774B2B9CD18F9175 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
| | | | | | | | | | | | | | | | | |
Db 233 CHHHSRVARMSDEFFPSMC 252

RESULT 11
Q52PY0_ECOLI
ID Q52PY0_ECOLI PRELIMINARY; PRT; 276 AA.
AC Q52PY0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Verocytotoxin 1 (Fragment).
GN Name=Vtl;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBi_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=378;
RA Catarame T.M.;
RT "Rapid Diagnostic Methods for food Borne Pathogens.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ537515; CAD6898.1; -; Genomic_DNA.
DR SMR; Q52PY0; 1-276.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
FT NON_TER 1 276
FT NON_TER 276 276
SQ SEQUENCE 276 AA; 30213 MW; 2BE68939E84D6378 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFPSMC 20
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Db 233 CHHHSRVARMSDEFFPSMC 252

RESULT 12
Q7WZ18_ECO57
ID Q7WZ18_ECO57 PRELIMINARY; PRT; 313 AA.
AC Q7WZ18;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Shiga toxin 1 variant A subunit.
GN Name=stx1;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBi_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AI2000/182;
RA Suzuki M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083043; BAC78637.1; -; Genomic_DNA.
DR HSSP; Q9FBI2; 1DM0.
DR SMR; Q7WZ18; 23-312.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
SQ SEQUENCE 313 AA; 34639 MW; DDF7ABF58F30BD19 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 313;

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Query Match          100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CHHHASRVARMASDEPPSMC 20
      |||||
DB      264 CHHHASRVARMASDEPPSMC 283

RESULT 14
SLTA_BPH30
ID SLTA_BPH30 STANDARD; PRT; 315 AA.
AC P10149;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-WAY-2005 (Rel. 47, Last annotation update)
DE Shiga toxin A-chain precursor (EC 3.2.2.22) (rRNA N-glycosidase).
GN Name-stxA;
OS Bacteriophage H30.
OC Viruses.
OX NCBI_TaxID=12371;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88139166; PubMed=2830229;
RA Strockbine N.A., Jackson M.P., Sung L.M., Holmes R.K., O'Brien A.D.;
RT "Cloning and sequencing of the genes for Shiga toxin from Shigella
RT dysenteriae type 1.";
RT J. Bacteriol. 170:1116-1122(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Kozlov Y.V., Kabishev A.A., Fedchenko V.I., Bayev A.A.;
RA "Cloning and primary structure of Shigella toxin genes.";
RT Dokl. Biochem. 295:744-749(1987).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89006281; PubMed=3049254; DOI=10.1016/0378-1119(88)90398-8;
RA Kozlov Y.V., Kabishev A.A., Lukyanov E.V., Bayev A.A.;
RT "The primary structure of the operons coding for Shigella dysenteriae
RT toxin and temperature phage H30 shiga-like toxin.";
RX Gene 67:213-221(1988).
RN CC
CC -!- FUNCTION: The A chain is responsible for inhibiting protein
CC synthesis through the catalytic inactivation of 60S ribosomal
CC subunits.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: Shiga toxin contains a single A-chain and five copies of
CC B-chain.
CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M19437; AAA98347.1; -; Genomic_DNA.
CC EMBL; X07903; CAA30741.1; -; Genomic_DNA.
CC EMBL; M24352; AAA26538.1; -; Genomic_DNA.
CC EMBL; M23980; AAA72732.1; -; Genomic_DNA.
CC SMR; P10149; 23-312.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00161; RIP; 1.
CC PROSITE; PS00275; SHIGA_RICIN; 1.
CC Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
FT SIGNAL
FT CHAIN 1 22 Shiga toxin A-chain.
FT ACT SITE 23 315 By similarity.
FT CONFLICT 67 67 T -> S (in Ref. 3).
FT CONFLICT 190 190 A -> P (in Ref. 2).
FT SEQUENCE 315 AA; 34814 MW; 8A423DF7ABF58F30 CRC64;

Query Match          100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFPSSMC 20  
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Db 264 CHHHSRVARMASDEFPSSMC 283

## RESULT 15

Q5MBW7\_9CAUD  
ID Q5MBW7\_9CAUD PRELIMINARY; PRT; 315 AA.  
AC Q5MBW7;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Stx1.  
GN Name=stx1;  
OS Stx1-converting phage phi-O153.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC Lambda-like viruses.  
OX NCBI\_TaxID=305853;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Karalius B.J., Butters J.R.;  
RT "Nucleotide sequence of stx region of Stx1-producing rabbit E. coli strain 0153:H-";  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY838795; AAW21758.1; -; Genomic\_DNA.  
DR SMR; Q5MBW7; 23-312.  
DR GO; GO:0016787; P:hydrolase activity; IEA.  
DR GO; GO:0030598; P:rRNA N-glycosylase activity; IEA.  
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PROSITE; PS00275; SHIGA RICIN; 1.  
KW Hydrolase; Protein synthesis inhibitor; Toxin.  
SQ SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;

Best Local Similarity 100.0%; Pred. No. 6.1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFPSSMC 20  
| | | | | | | | | | | | | | | | | |  
Db 264 CHHHSRVARMASDEFPSSMC 283

Search completed: February 10, 2006, 10:12:46

Job time : 18.9004 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:13:09 ; Search time 3.98524 Seconds  
(without alignments)  
414.909 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHNSRVARMSDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgm2\_6/ptodata/1/iaa/5 COMB.pcp.\*
- 2: /cgm2\_6/ptodata/1/iaa/6 COMB.pcp.\*
- 3: /cgm2\_6/ptodata/1/iaa/H COMB.pcp.\*
- 4: /cgm2\_6/ptodata/1/iaa/PCUS COMB.pcp.\*
- 5: /cgm2\_6/ptodata/1/iaa/RE COMB.pcp.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	20	1	US-07-988-430-58
2	114	100.0	20	1	US-08-425-336-56
3	114	100.0	20	1	US-08-488-113B-56
4	114	100.0	20	1	US-08-477-484B-56
5	114	100.0	20	1	US-08-646-360-56
6	114	100.0	20	2	US-08-839-765-56
7	114	100.0	20	2	US-09-136-389-56
8	114	100.0	20	2	US-09-610-838-56
9	114	100.0	20	2	US-09-711-485-56
10	114	100.0	20	4	PCT-US92-09487-58
11	114	100.0	315	1	US-08-378-761A-73
12	114	100.0	315	1	US-08-485-286-73
13	114	100.0	315	2	US-08-816-977-2
14	114	100.0	315	2	US-09-334-477-2
15	114	100.0	323	2	US-08-816-977-21
16	114	100.0	323	2	US-09-334-477-21
17	114	100.0	326	2	US-08-816-977-37
18	114	100.0	326	2	US-09-334-477-37
19	114	100.0	332	1	US-08-621-803-251
20	114	100.0	332	2	US-09-217-352-251
21	114	100.0	690	2	US-08-816-977-47
22	114	100.0	690	2	US-09-334-477-47
23	114	100.0	708	2	US-08-816-977-33
24	114	100.0	708	2	US-09-334-477-33
25	47	41.2	135	1	US-08-757-036-3
26	46	40.4	204	2	US-09-252-991A-18665
27	45	39.5	413	2	US-09-328-352-5860

28	45	39.5	525	2	US-09-252-991A-28266	Sequence 28266, A
29	44	38.6	138	1	US-08-757-036-1	Sequence 1, Appl
30	44	38.6	297	1	US-08-180-761B-2	Sequence 2, Appl
31	44	38.6	318	2	US-08-816-977-6	Sequence 6, Appl
32	44	38.6	318	2	US-09-334-477-6	Sequence 6, Appl
33	44	38.6	319	1	US-08-180-761B-1	Sequence 1, Appl
34	44	38.6	326	2	US-08-816-977-25	Sequence 25, Appl
35	44	38.6	326	2	US-09-334-477-25	Sequence 25, Appl
36	44	38.6	329	2	US-08-816-977-39	Sequence 39, Appl
37	44	38.6	329	2	US-09-334-477-39	Sequence 39, Appl
38	44	38.6	360	2	US-09-252-991A-28104	Sequence 28104, A
39	44	38.6	433	2	US-09-344-882-26	Sequence 26, Appl
40	44	38.6	433	2	US-10-293-865-26	Sequence 26, Appl
41	44	38.6	450	2	US-09-252-991A-24440	Sequence 24440, A
42	44	38.6	575	2	US-09-107-532A-3910	Sequence 49, Appl
43	44	38.6	694	2	US-08-816-977-49	Sequence 49, Appl
44	44	38.6	694	2	US-09-334-477-49	Sequence 49, Appl
45	44	38.6	711	2	US-08-816-977-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

US-07-988-430-58  
; Sequence 58, Application US/07988430  
; Patent No. 5416202  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen P.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,430  
; FILING DATE: 19921209  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5416202and, Greta E.  
; REGISTRATION NUMBER: 35302  
; REFERENCE/DOCKET NUMBER: 31133  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-988-430-58

Query Match 100.0%; Score 114; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFPSSMC 20  
Db 1 CHHHSRVARMASDEFPSSMC 20

## RESULT 2

US-08-425-336-56  
; Sequence 56, Application US/08425336  
; Patent No. 5621083  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/425,336  
; FILING DATE: 18-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Thomas C.  
; REGISTRATION NUMBER: P-36,989  
; REFERENCE/DOCKET NUMBER: 31394  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-425-336-56

Query Match 100.0%; Score 114; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFPSSMC 20  
Db 1 CHHHSRVARMASDEFPSSMC 20

## RESULT 3

US-08-488-113B-56  
; Sequence 56, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-488-113B-56

Query Match 100.0%; Score 114; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFPSSMC 20  
Db 1 CHHHSRVARMASDEFPSSMC 20

## RESULT 4

US-08-477-484B-56  
; Sequence 56, Application US/08477484B  
; Patent No. 5756699  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.



;; APPLICANT: Studnika, Gary M.  
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
;; TITLE OF INVENTION: Proteins  
;; NUMBER OF SEQUENCES: 169  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
;; STREET: 500 West Madison Street, 34th floor  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60661  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/477,484B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/425,336  
;; FILING DATE: 18-APR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/064,691  
;; FILING DATE: 12-MAY-1993  
;; APPLICATION NUMBER: US 07/988,430  
;; FILING DATE: 09-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 56:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-477-484B-56  
Query Match 100.0%; Score 114; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHHHSRVARMSDEFPFSC 20  
Db 1 CHHHSRVARMSDEFPFSC 20  
RESULT 5  
US-08-477-484B-56  
Sequence 56, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

;; STREET: 500 West Madison Street, 34th floor  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60661  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/646,360  
;; FILING DATE: 13-MAY-1996  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US94/05348  
;; FILING DATE: 12-MAY-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/064,691  
;; FILING DATE: 12-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/988,430  
;; FILING DATE: 09-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 200-70.P4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 56:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-646-360-56  
Query Match 100.0%; Score 114; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHHHSRVARMSDEFPFSC 20  
Db 1 CHHHSRVARMSDEFPFSC 20  
RESULT 6  
US-08-646-360-56  
Sequence 56, Application US/08839765  
Patent No. 6146631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-839-765-56

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Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CHHHSRVARMSDEFFPSMC 20
Db 1 CHHHSRVARMSDEFFPSMC 20

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RESULT 7
US-09-136-389-56
; Sequence 56, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-136-389-56

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Query Match 100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CHHHSRVARMSDEFFPSMC 20
Db 1 CHHHSRVARMSDEFFPSMC 20

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RESULT 8
US-09-610-838-56
; Sequence 56, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389

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; FILING DATE: 18-AUG-1998  
; APPLICATION NUMBER: 08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-610-838-56

Query Match 100.0%; Score 114; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPSC 20  
Db 1 CHHHSRVARMSDEFPSC 20

RESULT 9  
US-09-711-485-56  
; Sequence 56, Application US/09711485  
; Patent No. 6649742  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/711.485  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/839,765  
; FILING DATE:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-711-485-56

Query Match 100.0%; Score 114; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPSC 20  
Db 1 CHHHSRVARMSDEFPSC 20

## RESULT 10

PCT-US92-09487-58  
; Sequence 58, Application PC/TUS9209487  
; GENERAL INFORMATION:  
; APPLICANT: Bernhardt, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09487  
; FILING DATE: 19921104  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:

```
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35302
;; REFERENCE/DOCKET NUMBER: 31133
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 346-5750
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US92-09487-58

Query Match 100.0%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFPSMC 20
Db 1 CHHHSRVARWASDEFFPSMC 20

RESULT 11
US-08-378-761A-73
; Sequence 73, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-73

Query Match 100.0%; Score 114; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFPSMC 20
Db 264 CHHHSRVARWASDEFFPSMC 283

RESULT 13
US-08-816-977-2
; Sequence 2, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Byrnie, Lisa M.
; APPLICANT: Pugh, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; TITLE OF INVENTION: Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
```

CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,977  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-977-2

Query Match 100.0%; Score 114; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 5.5e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20  
Db 264 CHHHSRVARMASDEFFSMC 283

RESULT 14  
US-09-334-477-2  
Sequence 2, Application US/09334477  
Patent No. 6652857  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
Byrne, Lisa M.  
Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/334,477  
FILING DATE: 16-Jun-1999  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,977  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-334-477-2

Query Match 100.0%; Score 114; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 5.5e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20  
Db 264 CHHHSRVARMASDEFFSMC 283

RESULT 15  
US-08-816-977-21  
Sequence 21, Application US/08816977  
Patent No. 6080400  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
APPLICANT: Byrne, Lisa M.  
APPLICANT: Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,977  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-977-21

Query Match 100.0%; Score 114; DB 2; Length 323;  
Best Local Similarity 100.0%; Pred. No. 5.6e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMASDEFFSMC 20  
Db 264 CHHHSRVARMASDEFFSMC 283

Search completed: February 10, 2006, 10:15:58  
Job time : 4.98524 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 13.0627 Seconds  
(without alignments)  
639.727 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHRSRVARWASDEFPSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	20	4	US-10-127-890-56
2	114	100.0	20	5	US-10-717-243-56
3	114	100.0	293	3	US-09-792-793A-37
4	114	100.0	293	4	US-10-375-209A-37
5	114	100.0	315	3	US-09-334-477-2
6	114	100.0	323	3	US-09-334-477-21
7	114	100.0	326	3	US-09-334-477-37
8	114	100.0	332	3	US-09-765-527-251
9	114	100.0	690	3	US-09-334-477-47
10	114	100.0	708	3	US-09-334-477-33
11	48	42.1	96	4	US-10-425-115-237717
12	48	42.1	162	4	US-10-767-701-40168
13	47	41.2	74	4	US-10-424-599-224605
14	47	41.2	135	3	US-09-962-021-3
15	47	41.2	135	4	US-10-408-765A-20
16	47	41.2	293	5	US-10-732-923-4254
17	47	41.2	294	4	US-10-437-963-194718
18	46.5	40.8	345	4	US-10-424-599-200140
19	46	40.4	19	5	US-10-502-882-10
20	46	40.4	196	4	US-10-282-122A-66424
21	45	39.5	380	4	US-10-437-963-116579
22	44.5	39.0	250	4	US-10-369-493-10325
23	44.5	39.0	275	4	US-10-425-115-220907
24	44.5	39.0	280	4	US-10-425-114-52863
25	44.5	39.0	544	3	US-09-925-299-1004
26	44.5	39.0	544	3	US-09-925-299-1004
27	44	38.6	82	4	US-10-424-599-216625

28 44 38.6 137 4 US-10-408-765A-1100 Sequence 1100, Ap  
29 44 38.6 138 3 US-09-962-021-1 Sequence 1, Appli  
30 44 38.6 249 4 US-10-156-761-13851 Sequence 13851, A  
31 44 38.6 286 5 US-10-732-923-14451 Sequence 14451, A  
32 44 38.6 293 4 US-10-424-599-223435 Sequence 223435,  
33 44 38.6 318 3 US-09-334-477-6 Sequence 6, Appli  
34 44 38.6 319 3 US-09-792-793A-38 Sequence 38, Appl  
35 44 38.6 319 3 US-09-870-759-28 Sequence 28, Appl  
36 44 38.6 319 3 US-09-751-708A-28 Sequence 28, Appl  
37 44 38.6 319 4 US-10-375-209A-38 Sequence 38, Appl  
38 44 38.6 319 4 US-10-428-817A-24 Sequence 24, Appl  
39 44 38.6 319 5 US-10-937-758A-28 Sequence 28, Appl  
40 44 38.6 326 3 US-09-334-477-25 Sequence 25, Appl  
41 44 38.6 329 3 US-09-334-477-39 Sequence 39, Appl  
42 44 38.6 427 4 US-10-437-963-106648 Sequence 106648,  
43 44 38.6 433 3 US-09-344-882-26 Sequence 26, Appl  
44 44 38.6 433 4 US-10-293-865-26 Sequence 26, Appl  
45

#### ALIGNMENTS

#### RESULT 1

US-10-127-890-56  
; Sequence 56, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127,890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-127-890-56

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Query Match      100.0%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CHHHSRVARMASDDEFPSC 20  
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Db 1 CHHHSRVARMASDDEFPSC 20

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RESULT 2
US-10-717-243-56
; Sequence 56, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
;           Carroll, Stephen F.
;           Studnika, Gaty M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-NOV-2003
CLASSIFICATION: 530

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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 368-1248  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-10-717-243-56

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Query Match      100.0%; Score 114; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CHHHSRVARMSDEFPSMC 20  
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db 1 CHHHSRVARMSDEFPSMC 20

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RESULT 3
US-09-792-793A-37
; Sequence 37, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: OTHER INFLAMMATORY
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Shigella dysenteriae
US-09-792-793A-37

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Query Match      100.0%; Score 114; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CHHASRVARMASDEFPSC 20  
Db 242 CHHASRVARMASDEFPSC 261

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RESULT 4
US-10-375-209A-37
; Sequence 37, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogswins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF INFLAMMATORY DISEASES
; TITLE OF INVENTION: OTHER INFLAMMATORY DISEASES
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375-209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 293
; TYPE: prt
; ORGANISM: Shigella dysenteriae
US-10-375-209A-37

```

```
Query Match      100.0%; Score 114; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CHHHSRVARMASDEFPSC 20  
|||  
Db 242 CHHHSRVARMASDEFPSC 261

RESULT 5  
US-09-334-477-2  
; Sequence 2, Application US/09334477  
; Patent No. US20020012658A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, James A.



Byrne, Lisa M.  
Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/334,477  
FILING DATE: 16-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,977  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-334-477-2  
Query Match 100.0%; Score 114; DB 3; Length 315;  
Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHHHSRVARMSDEFPSMC 20  
Db 264 CHHHSRVARMSDEFPSMC 283  
RESULT 6  
US-09-334-477-21  
Sequence 21, Application US/09334477  
Patent No. US200200126581  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
Byrne, Lisa M.  
Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/334,477  
FILING DATE: 16-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,977  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-334-477-21  
Query Match 100.0%; Score 114; DB 3; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.9e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CHHHSRVARMSDEFPSMC 20  
Db 264 CHHHSRVARMSDEFPSMC 283  
RESULT 7  
US-09-334-477-37  
Sequence 37, Application US/09334477  
Patent No. US200200126581  
GENERAL INFORMATION:  
APPLICANT: Williams, James A.  
Byrne, Lisa M.  
Pugh, Charles S.G.  
TITLE OF INVENTION: Prevention And Treatment Of  
Verotoxin-Induced Disease  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/334,477  
FILING DATE: 16-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,977  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: OPHD-02450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 327 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

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;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-334-477-37

Query Match          100.0%; Score 114; DB 3; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFSMC 20
Db 275 CHHHSRVARMSDEFFSMC 294

RESULT 8
US-09-765-527-251
; Sequence 251, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251

Query Match          100.0%; Score 114; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFSMC 20
Db 277 CHHHSRVARMSDEFFSMC 296

RESULT 9
US-09-334-477-47
; Sequence 47, Application US/09334477
; Patent No. US2002012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; BYRNE, Lisa M.
; PUGH, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
; FILING DATE: 16-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/816,977
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: OPHD-02450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-334-477-47

Query Match          100.0%; Score 114; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFFSMC 20
Db 639 CHHHSRVARMSDEFFSMC 658

RESULT 10
US-09-334-477-33
; Sequence 33, Application US/09334477
; Patent No. US2002012658A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; BYRNE, Lisa M.
; PUGH, Charles S.G.
; TITLE OF INVENTION: Prevention And Treatment Of
; Verotoxin-Induced Disease
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,477
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; FILING DATE: 16-Jun-1999  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/816,977  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: OPD-02450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 709 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-334-477-33

Query Match 100.0%; Score 114; DB 3; Length 708;  
Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPSC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 657 CHHHSRVARMSDEFPSC 676

RESULT 11  
US-10-425-115-237717  
; Sequence 237717, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 237717  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_148383C.1.pep  
US-10-425-115-237717

Query Match 42.1%; Score 48; DB 4; Length 96;  
Best Local Similarity 50.0%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSD 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 82 CHHHLRLSGSAID 95

RESULT 12  
US-10-767-701-40168  
; Sequence 40168, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 40168  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C46914\_1.pep  
US-10-767-701-40168

Query Match 42.1%; Score 48; DB 4; Length 162;  
Best Local Similarity 44.4%; Pred. No. 19;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CHHHSRVARMSDEFPSS 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 44 CYHHHDNYATVSTDFFS 61

RESULT 13  
US-10-424-599-224605  
; Sequence 224605, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 224605  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_44849C.1.pep  
US-10-424-599-224605

Query Match 41.2%; Score 47; DB 4; Length 74;  
Best Local Similarity 50.0%; Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 HHHSRVARMSDEFP 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 58 HGHGSKVSTLASSNFP 73

RESULT 14  
US-09-962-021-3  
; Sequence 3, Application US/09962021  
; Patent No. US20020106737A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Goli, Surya K.  
; TITLE OF INVENTION: HUMAN SOM1 PROTEIN HOMOLOG  
; FILE REFERENCE: PF-0170-2 CON  
; CURRENT APPLICATION NUMBER: US/09/962,021  
; CURRENT FILING DATE: 2001-09-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020106737A1 g180233  
US-09-962-021-3

Query Match 41.2%; Score 47; DB 3; Length 135;  
Best Local Similarity 44.4%; Pred. No. 22;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFFS 18  
||| | : | |||  
Db 58 CAHLIRLLKCKRDSFPS 75

RESULT 15  
US-10-408-765A-20  
; Sequence 20, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-20

Query Match 41.2%; Score 47; DB 4; Length 135;  
Best Local Similarity 44.4%; Pred. No. 22;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CHHHSRVARMSDEFFS 18  
||| | : | |||  
Db 58 CAHLIRLLKCKRDSFPS 75

Search completed: February 10, 2006, 10:44:46  
Job time : 14.0627 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:39:04 ; Search time 1.03321 Seconds  
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254.015 Million cell updates/sec

Title: US-10-717-243-56

Perfect score: 114

Sequence: 1 CHHHSRVARWASDEFFSMC 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pap.\*  
2: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pap.\*  
3: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pap.\*  
4: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pap.\*  
5: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pap.\*  
6: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pap.\*  
7: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pap.\*  
8: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	315	7	US-11-010-795-28
2	44	38.6	319	7	US-11-010-795-26
3	44	38.6	433	7	US-11-167-856-26
4	43	37.7	541	7	US-11-059-814-20
5	40	35.1	493	7	US-11-010-239-81
6	39	34.2	205	6	US-10-793-626-1828
7	39	34.2	263	6	US-10-793-626-1418
8	39	34.2	285	7	US-11-094-519A-36
9	39	34.2	399	7	US-11-094-519A-37
10	39	34.2	402	6	US-10-821-234-1581
11	39	34.2	502	7	US-11-111-664-6
12	39	34.2	512	7	US-11-111-664-8
13	38	33.3	304	6	US-10-793-626-1530
14	38	33.3	423	6	US-10-883-512-76
15	38	33.3	559	6	US-10-521-162-4
16	38	33.3	699	7	US-11-138-642-4
17	38	33.3	699	7	US-11-138-882-4
18	38	33.3	712	6	US-10-521-162-12
19	37.5	32.9	244	6	US-10-467-657-2638
20	37	32.5	146	7	US-11-226-657-63
21	37	32.5	259	7	US-11-156-084-326
22	37	32.5	306	7	US-11-152-569-19
23	37	32.5	486	6	US-10-877-346-50
24	37	32.5	569	6	US-10-632-150-2
25	37	32.5	569	7	US-11-073-457-2

Sequence 12, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 1150, Ap  
Sequence 1209, Ap  
Sequence 1144, Ap  
Sequence 1154, Ap  
Sequence 1152, Ap  
Sequence 10, Appl  
Sequence 241, App  
Sequence 319, App  
Sequence 2886, Ap  
Sequence 147, App  
Sequence 4, Appl  
Sequence 8, Appl  
Sequence 108, App  
Sequence 106, App

26 37 32.5 569 7 US-11-039-691-12  
27 37 32.5 569 7 US-11-073-460-2  
28 37 32.5 798 7 US-11-107-028-3  
29 37 32.5 954 6 US-10-453-372-1150  
30 37 32.5 1189 6 US-10-821-234-1209  
31 37 32.5 1268 6 US-10-453-372-1144  
32 37 32.5 1268 6 US-10-453-372-1154  
33 37 32.5 1288 6 US-10-453-372-1146  
34 37 32.5 1288 6 US-10-453-372-1152  
35 37 32.5 1766 7 US-11-075-185-10  
36 36 31.6 19 6 US-10-939-890-241  
37 36 31.6 227 7 US-11-052-554A-319  
38 36 31.6 277 6 US-10-467-657-2886  
39 36 31.6 419 7 US-11-166-993-147  
40 36 31.6 604 7 US-11-183-136-4  
41 36 31.6 604 7 US-11-046-653-1  
42 36 31.6 832 7 US-11-182-016-8  
43 36 31.6 1017 7 US-11-054-281-108  
44 36 31.6 1219 7 US-11-054-281-28  
45 36 31.6 1219 7 US-11-054-281-106

## ALIGNMENTS

## RESULT 1

US-11-010-795-28  
; Sequence 28, Application US/11010795  
; Publication No. US20060005271A1  
; GENERAL INFORMATION:  
; APPLICANT: TUMER, NILGUN E.  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE  
; FILE REFERENCE: OCIRS 3.0-085  
; CURRENT APPLICATION NUMBER: US/11/010,795  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: 60/529,348  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 28  
; LENGTH: 315  
; TYPE: PRT  
; ORGANISM: Bacteriophage SC370  
US-11-010-795-28

Query Match 100.0%; Score 114; DB 7; Length 315;  
Best Local Similarity 100.0%; Pred. No. 2.2e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHSRVARWASDEFFSMC 20  
Db 264 CHHHSRVARWASDEFFSMC 283

## RESULT 2

US-11-010-795-26  
; Sequence 26, Application US/11010795  
; Publication No. US20060005271A1  
; GENERAL INFORMATION:  
; APPLICANT: TUMER, NILGUN E.  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE  
; FILE REFERENCE: OCIRS 3.0-085  
; CURRENT APPLICATION NUMBER: US/11/010,795  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: 60/529,348  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 26

```

; LENGTH: 319
; TYPE: PRT
; ORGANISM: Bacteriophage SC370
US-11-010-795-26

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Query Match 38.6%; Score 44; DB 7; Length 319;  
Best Local Similarity 35.0%; Pred. No. 4.8;  
Matches 7; Conservative 3; Mismatches 10; Indels

QY 1 CHHHSRVARMASDEFPSMC 20  
||| : | | :: |  
Db 263 CHHOGARSVRVAVNEESOPC 282

### RESULT 3

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US-11-167-856-26
; Sequence 26, Application US/11167856
; Publication No. US20050268352A1
; GENERAL INFORMATION:
; APPLICANT: Nikolau, Basil J
; APPLICANT: Wuterle, Eve S
; APPLICANT: Oliver, David J
; APPLICANT: Behal, Robert
; APPLICANT: Schnable, Patrick S
; APPLICANT: Ke, Jinshan
; APPLICANT: Johnson, Jerry L
; APPLICANT: Allred, Carolyn C
; APPLICANT: Farland, Beth
; APPLICANT: Lutziger, Isabelle
; APPLICANT: Wen, Tsui-Jung
; TITLE OF INVENTION: Materials and Methods for
; TITLE OF INVENTION: Acetyl CoA Lev
; FILE REFERENCE: P2194USD-2

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Query Match 38.6%; Score 44; DB 7; Length 433;  
Best Local Similarity 41.2%; Pred. No. 6.5;  
Matches 7; Conservative 5; Mismatches 5; Indels

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Qy      3 HHASRVARMASDEFFSM 19
        || |::| | |::
Db     265 HHVQRLSRLLSDPRPTI 281
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## RESULT 4

```

RESUBMIT - 05
US-11-059-814-20
; Sequence 20, Application US/11059814
; Publication No. US20050273650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods
; TITLE OF INVENTION: Proliferation Disord
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-814-20

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Query Match 37.7%; Score 43; DB 7; Length 541;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 8: Conservative 2; Mismatches 4; Indels

Qy 2 HHASRVARMASDE 15  
||| ||| : ||:  
pb 194 HHWSRAALVYSDD 207

RESIT.T 5

```

RESUME 3
US-11-010-239-81
; Sequence 81, Application US/11010239
; Publication No. US20060015970A1
; GENERAL INFORMATION:
; APPLICANT: Roger PENNELL
; APPLICANT: Jack OKAMURO
; APPLICANT: Richard SCHNEBERGER
; APPLICANT: Yiwen FANG
; APPLICANT: Shing KWOK
; APPLICANT: Diane JOFUKU
; APPLICANT: Edward A. KIEGLE
; APPLICANT: Jonathan DONSON
; APPLICANT: Nestor APUYA
; TITLE OF INVENTION: NUCLEOTIDE SEQU
; TITLE OF INVENTION: MODIFYING PLAN
; FILE REFERENCE: 2750-1585PUS2
; CURRENT APPLICATION NUMBER: US/11/0
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: US 60/529
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(493)
; OTHER INFORMATION: 13609817_protei
US-11-010-239-81

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Query Match 35.1%; Score 40; DB 7; Length 493;  
Best Local Similarity 46.7%; Pred. No. 33;  
Matches 7; Conservative 3; Mismatches 5; Indels

```

QY      2 HHHASRVARMASDEF 16
        ||| :| :| :|
Db     14 HHHGHQVFDVASHDF 28

```

## RESULT 6

US-10-793-626-1828  
 ; Sequence 1828, Application US/10793626  
 ; Publication No. US20050255478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PU3480US  
 ; CURRENT APPLICATION NUMBER: US/10/793,626  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: 60/164,258  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1828

; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1828

Query Match 34.2%; Score 39; DB 6; Length 205;  
Best Local Similarity 57.1%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEF 16  
||| ||| ||| |||  
Db 19 HHGKAVKRGASDTF 32

RESULT 7  
US-10-793-626-1418  
; Sequence 1418, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PUS3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1418  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1418

Query Match 34.2%; Score 39; DB 6; Length 263;  
Best Local Similarity 57.1%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 HHASRVARMASDEF 16  
||| ||| ||| |||  
Db 56 HHGKAVKRGASDTF 69

RESULT 8  
US-11-094-519A-36  
; Sequence 36, Application US/11094519A  
; Publication No. US20050281810A1  
; GENERAL INFORMATION:  
; APPLICANT: BERNSTEIN, Jeanne  
; APPLICANT: LEVINE, Zurit  
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING  
; FILE REFERENCE: 2786-0140P  
; CURRENT APPLICATION NUMBER: US/11/094,519A  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR APPLICATION NUMBER: US/09/695,293  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: IL 132558  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-094-519A-36

Query Match 34.2%; Score 39; DB 7; Length 285;

Best Local Similarity 61.5%; Pred. No. 28;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHASRVARMASD 14  
||| ||| ||| |||  
Db 25 HHPPSYVAHLASD 37

RESULT 9  
US-11-094-519A-37  
; Sequence 37, Application US/11094519A  
; Publication No. US20050281810A1  
; GENERAL INFORMATION:  
; APPLICANT: BERNSTEIN, Jeanne  
; APPLICANT: LEVINE, Zurit  
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING  
; FILE REFERENCE: 2786-0140P  
; CURRENT APPLICATION NUMBER: US/11/094,519A  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR APPLICATION NUMBER: US/09/695,293  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: IL 132558  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 399  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-094-519A-37

Query Match 34.2%; Score 39; DB 7; Length 399;  
Best Local Similarity 61.5%; Pred. No. 39;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHASRVARMASD 14  
||| ||| ||| |||  
Db 25 HHPPSYVAHLASD 37

RESULT 10  
US-10-821-234-1581  
; Sequence 1581, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: dt\_seq\_genes Version 1.0  
; SEQ ID NO 1581  
; LENGTH: 402  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1581

Query Match 34.2%; Score 39; DB 6; Length 402;  
Best Local Similarity 61.5%; Pred. No. 39;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 HHASRVARMASD 14  
||| ||| ||| |||  
Db 25 HHPPSYVAHLASD 37

RESULT 11

US-11-111-664-6  
; Sequence 6, Application US/11111664  
; Publication No. US20060014687A1  
; GENERAL INFORMATION:  
; APPLICANT: ENOBIA PHARMA INC.  
; APPLICANT: Crine, Philippe  
; APPLICANT: Loisel, Thomas  
; APPLICANT: Lemire, Isabelle  
; APPLICANT: Boileau, Guy  
; TITLE OF INVENTION: BONE DELIVERY CONJUGATES AND METHOD OF USING SAME TO TARGET  
; FILE REFERENCE: 2006078-0003  
; CURRENT APPLICATION NUMBER: US/11/111,664  
; CURRENT FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: US 60/563,828  
; PRIOR FILING DATE: 2004-04-21  
; PRIOR APPLICATION NUMBER: US 60/614,984  
; PRIOR FILING DATE: 2004-10-04  
; PRIOR APPLICATION NUMBER: US 60/590,347  
; PRIOR FILING DATE: 2004-07-23  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Soluble alkaline phosphatase  
US-11-111-664-6  
Query Match 34.2%; Score 39; DB 7; Length 502;  
Best Local Similarity 37.5%; Pred. No. 49;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 2 HHASRVARMASDEFP 17  
||: ||: ||:  
Db 78 HNPGEETRLMDKFP 93  
  
RESULT 12  
US-11-111-664-8  
; Sequence 8, Application US/11111664  
; Publication No. US20060014687A1  
; GENERAL INFORMATION:  
; APPLICANT: ENOBIA PHARMA INC.  
; APPLICANT: Crine, Philippe  
; APPLICANT: Loisel, Thomas  
; APPLICANT: Lemire, Isabelle  
; APPLICANT: Boileau, Guy  
; TITLE OF INVENTION: BONE DELIVERY CONJUGATES AND METHOD OF USING SAME TO TARGET  
; FILE REFERENCE: 2006078-0003  
; CURRENT APPLICATION NUMBER: US/11/111,664  
; CURRENT FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: US 60/563,828  
; PRIOR FILING DATE: 2004-04-21  
; PRIOR APPLICATION NUMBER: US 60/614,984  
; PRIOR FILING DATE: 2004-10-04  
; PRIOR APPLICATION NUMBER: US 60/590,347  
; PRIOR FILING DATE: 2004-07-23  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 512  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Soluble alkaline phosphatase conjugate  
US-11-111-664-8  
Query Match 34.2%; Score 39; DB 7; Length 512;  
Best Local Similarity 37.5%; Pred. No. 50;  
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 HHASRVARMASDEFP 17  
||: ||: ||:  
Db 78 HNPGEETRLMDKFP 93  
  
RESULT 13  
US-10-793-626-1530  
; Sequence 1530, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1530  
; LENGTH: 304  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1530  
Query Match 33.3%; Score 38; DB 6; Length 304;  
Best Local Similarity 43.8%; Pred. No. 43;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 3 HHASRVARMASDEFP 18  
||: ||: ||:  
Db 88 HHAYRILRAVKNRFGS 103  
  
RESULT 14  
US-10-883-512-76  
; Sequence 76, Application US/10883512  
; Publication No. US20060005265A1  
; GENERAL INFORMATION:  
; APPLICANT: Bughara, Suleiman  
; APPLICANT: Han, Zhao  
; TITLE OF INVENTION: Rvegrass CBF3 Gene: Identification and Isolation  
; FILE REFERENCE: MSU-08807  
; CURRENT APPLICATION NUMBER: US/10/883,512  
; CURRENT FILING DATE: 2004-07-01  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 76  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-883-512-76  
Query Match 33.3%; Score 38; DB 6; Length 423;  
Best Local Similarity 38.9%; Pred. No. 60;  
Matches 7; Conservative 2; Mismatches 9; Indels 0; Gaps 0;  
  
Qy 2 HHASRVARMASDEFP 19  
||: ||: ||:  
Db 36 HHRDRDLDAISAISLPSV 53  
  
RESULT 15  
US-10-521-162-4  
; Sequence 4, Application US/10521162  
; Publication No. US20050287529A1  
; GENERAL INFORMATION:  
; APPLICANT: Brandt, Kevin S.



; TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,  
; TITLE OF INVENTION: PROTEINS AND USES THEREOF  
; FILE REFERENCE: FC-11-PCT  
; CURRENT APPLICATION NUMBER: US/10/521,162  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: 60/319,402  
; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: 60/426,601  
; PRIOR FILING DATE: 2003-11-15  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 559  
; TYPE: PRT  
; ORGANISM: Ctenocephalides felis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (192)..(192)  
; OTHER INFORMATION: The 'Xaa' at location 192 stands for Ala, or Thr.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (193)..(193)  
; OTHER INFORMATION: The 'Xaa' at location 193 stands for Asn, or Tyr.  
US-10-521-162-4

Query Match 33.3%; Score 38; DB 6; Length 559;  
Best Local Similarity 83.3%; Pred. No. 79;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHHS 6  
Db 140 CHHSS 145

Search completed: February 10, 2006, 10:45:19  
Job time : 1.03321 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 10.8856 Seconds  
(without alignments)  
807.265 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSCQAGAAASELFSINHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	20	2	AAR37301 Rabbit Mu
2	99	99.0	153	5	Abp42706 Human ova
3	99	99.0	363	2	Aay07116 Lung canc
4	99	99.0	364	2	Aay06992 Glycolyti
5	99	99.0	364	7	Adf76857 Novel hum
6	99	99.0	364	7	Adf68731 Human hea
7	99	99.0	364	8	Adf77178 Human pro
8	99	99.0	364	8	Adi02918 Human fru
9	99	99.0	364	8	Adq76754 Human fru
10	99	99.0	364	8	Adm81754 Tumour-as
11	99	99.0	364	8	Adu46860 Aldolase
12	99	99.0	364	9	Adx05876 Cyclin-de
13	99	99.0	364	9	Adz70640 Human pro
14	99	99.0	364	9	Adz70327 Human pro
15	97	97.0	22	9	Adv50900 Murine br
16	97	97.0	364	7	Adb79827 Rat aldol
17	95	95.0	31	3	AAb44017 Human can
18	68	68.0	363	9	Adw08677 Human pro
19	68	68.0	364	5	Abp65148 Hypoxia-r
20	68	68.0	364	7	Adj68292 Human hea
21	68	68.0	364	8	Adl12661 Human ste
22	61	61.0	365	8	Adn23270 Bacterial
23	55.5	55.5	361	4	Abb66969 Drosophil
24	52	52.0	366	8	Adn23082 Bacterial

25	51	51.0	371	8	ADY10167	Ady10167 Plant ful
26	50.5	50.5	215	8	ABO60233	ABO60233 Human gen
27	50.5	50.5	836	7	ABR83671	ABR83671 Human bkl
28	50.5	50.5	836	7	ADM05015	ADM05015 Human pro
29	50.5	50.5	836	8	ADO85827	ADO85827 Different
30	48	48.0	1772	8	ADR12606	ADR12606 Gene vacc
31	47	47.0	1223	4	ABB63399	ABB63399 Drosophil
32	46	46.0	9	8	ADN63558	ADN63558 HLA bindi
33	46	46.0	9	8	ADN64270	ADN64270 HLA bindi
34	46	46.0	132	6	ABP96323	ABP96323 Human AGE
35	46	46.0	170	6	ABU01993	ABU01993 S. pneumo
36	46	46.0	170	8	ADR46838	ADR46838 Streptoco
37	46	46.0	171	8	ADR95229	ADR95229 Novel S.
38	46	46.0	171	9	AEA59099	AEA59099 Streptoco
39	46	46.0	283	4	AAW93735	AAW93735 Human pol
40	46	46.0	283	8	ADL31668	ADL31668 Human pro
41	46	46.0	292	6	AAO19583	AAO19583 Human pro
42	46	46.0	292	6	ABB99461	ABB99461 Protein 5
43	46	46.0	295	8	AAO19582	AAO19582 Human pro
44	46	46.0	295	8	ADR10068	ADR10068 Human pro
45	46	46.0	324	5	ABP69378	ABP69378 Human pol

#### ALIGNMENTS

#### RESULT 1

AAR37301  
ID AAR37301 standard; protein; 20 AA.

XX AAR37301;

AC AAR37301;

XX 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

DT 13-SEP-1993 (first entry)

XX Rabbit Muscle aldolase peptide segment.

XX Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;

KW autoimmune disease; cell killing; toxin; human engineered antibody;

KW variable region; light chain; cell targeting; chimeric antibody; RMA;

KW linker.

XX Oryctolagus cuniculus.

OS Oryctolagus cuniculus.

XX Key Location/Qualifiers

FT Cleavage-site 1..20

FT /note= "contains several potential cathepsin cleavage

FT Sites"

XX WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA ) XOMA CORP.

XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic

FT agents, immuno toxins for treating auto immune diseases, cancer, graft

FT versus host disease and selective cell killing in-vivo.

XX Example 10; Page 115; 163pp; English.

XX The invention covers analogues of the plant type I RIP gelonin which have

CC a non-naturally occurring Cys residue in a position which enables the

CC analogue to be conjugated via a disulphide linkage to a molecule which

CC specifically binds to a target cell. Pref. target-cell binding molecules  
 CC are antibodies or their fragments, esp. human engineered H65 antibody  
 CC fragments. Fusion constructs were assembled that included a natural  
 CC sequence gelonin gene fused to an H65 truncated heavy chain gene or an  
 CC H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of  
 CC the rabbit muscle aldolase was inserted between the gelonin gene and the  
 CC Ab gene. The resulting immunoconjugates can be used as cytotoxic  
 CC therapeutic agents. (Updated on 25-MAR-2003 to correct FN field.)  
 XX  
 SQ Sequence 20 AA;  
 Query Match 100.0%; Score 100; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-10; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PSGQAGAAASESLFISNHAY 20  
 Db 1 PSGQAGAAASESLFISNHAY 20  
 RESULT 2  
 ID ABP42706 standard; protein; 153 AA.  
 AC ABP42706;  
 XX  
 DT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HOPKN14, SEQ ID NO:3838.  
 XX  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FN WO200200677-A1.  
 XX  
 XX 03-JAN-2002.  
 XX  
 XX 07-JUN-2001; 2001WO-US018569.  
 XX  
 XX 07-JUN-2000; 2000US-0209467P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Birse CE, Rosen CA;  
 XX  
 XX WPI; 2002-147878/19.  
 DR N-PSDB; ABQ55783.  
 DR  
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 XX cancer), immune disorders, cardiovascular disorders and neurological  
 XX diseases.  
 XX  
 XX Claim 11; SEQ ID NO 3838; 2922pp; English.  
 XX  
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 XX encompasses polypeptides 90% identical and polynucleotides 95% identical  
 XX to the sequences of the invention. The invention additionally relates to  
 XX recombinant vectors and host cells comprising human ovarian antigen  
 XX polynucleotides, antibodies against human ovarian antigens, and the use  
 XX of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 XX treating, prognosing or preventing various ovary and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 153 AA;  
 Query Match 99.0%; Score 99; DB 5; Length 153;  
 Best Local Similarity 95.0%; Pred. No. 1.5e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PSGQAGAAASESLFISNHAY 20  
 Db 134 PSGQAGAAASESLFISNHAY 153  
 RESULT 3  
 AAY07116  
 ID AAY07116 standard; protein; 363 AA.  
 XX  
 AC AAY07116;  
 XX  
 DT 02-JUL-1999 (first entry)  
 XX  
 DE Lung cancer associated antigen precursor sequence.  
 XX  
 KW Cancer associated antigen; diagnosis; research; treatment; human;  
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;  
 KW prostate cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9904265-A2.  
 XX  
 XX 28-JAN-1999.  
 XX  
 XX 15-JUL-1998; 98WO-US014679.  
 XX  
 XX 17-JUL-1997; 97US-00896164.  
 PR 10-OCT-1997; 97US-0061599P.  
 PR 10-OCT-1997; 97US-0061765P.  
 PR 10-OCT-1997; 97US-00948705.  
 PR 11-OCT-1997; 97GB-00021697.  
 PR 22-JUN-1998; 98US-00102322.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;  
 PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;  
 XX  
 XX WPI; 1999-132448/11.  
 DR  
 XX New isolated cancer associated nucleic acids and polypeptides - isolated  
 XX using sera from cancer patients, used to develop products for the  
 XX diagnosis, monitoring or treatment of cancers.

PS Disclosure; Page 733-734; 787pp; English.

XX The invention relates to a method for diagnosing a disorder characterised  
 CC by expression of a human cancer associated antigen precursor coded for by  
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
 CC biological sample isolated from a subject with an agent that specifically  
 CC binds to the NAM, an expression product or a fragment of an expression  
 CC product complexed with an HLA molecule; and (b) determining the  
 CC interaction between the agent and the NAM or the expression product as a  
 CC determination of the disorder. The products and methods can be used in  
 CC the diagnosis, monitoring, research, or treatment of conditions  
 CC characterised by the expression of various cancer associated antigens.  
 CC The invention provides nucleic acid sequences and encoded polypeptides  
 CC which are cancer associated antigen precursors expressed in human breast  
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
 CC lung cancer

XX Sequence 363 AA;

Query Match 99.0%; Score 99; DB 2; Length 363;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFVSNHAY 20

Db 344 PSGQAGAAASESLFVSNHAY 363

RESULT 4

AAy06992  
 ID AAY06992 standard; protein; 364 AA.

XX AC AAY06992;

XX DT 02-JUL-1999 (first entry)

XX DE Glycolytic enzyme aldolase A.

XX KW Cancer associated antigen; diagnosis; research; treatment; human;  
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;  
 KW prostate cancer.

XX OS Homo sapiens.

XX PN WO9904265-A2.

XX PD 28-JAN-1999.

XX PP 15-JUL-1998; 98WO-US014679.

XX PR 17-JUL-1997; 97US-00896164.

XX PR 10-OCT-1997; 97US-0061599P.

XX PR 10-OCT-1997; 97US-0061765P.

XX PR 10-OCT-1997; 97US-00948705.

XX PR 11-OCT-1997; 97GB-00021697.

XX PR 22-JUN-1998; 98US-00102322.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;

XX PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;

XX DR WPI; 1999-132448/11.

XX DR N-PSDB; AAX40193.

XX New isolated cancer associated nucleic acids and polypeptides - isolated  
 PT using sera from cancer patients, used to develop products for the  
 PT diagnosis, monitoring or treatment of cancers.

XX Example 8; Page 769-770; 787pp; English.

XX The invention relates to a method for diagnosing a disorder characterised  
 CC by expression of a human cancer associated antigen precursor coded for by

CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
 CC biological sample isolated from a subject with an agent that specifically  
 CC binds to the NAM, an expression product or a fragment of an expression  
 CC product complexed with an HLA molecule; and (b) determining the  
 CC interaction between the agent and the NAM or the expression product as a  
 CC determination of the disorder. The products and methods can be used in  
 CC the diagnosis, monitoring, research, or treatment of conditions  
 CC characterised by the expression of various cancer associated antigens.  
 CC The invention provides nucleic acid sequences and encoded polypeptides  
 CC which are cancer associated antigen precursors expressed in human breast  
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
 CC lung cancer

XX Sequence 364 AA;

Query Match 99.0%; Score 99; DB 2; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFVSNHAY 20

Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 5

ADP76857  
 ID ADP76857 standard; protein; 364 AA.

XX AC ADP76857;

XX DT 26-FEB-2004 (first entry)

XX DE Novel human secreted and transmembrane protein SeqID 532.

XX KW human; PRO; membrane bound protein; membrane bound receptor;  
 KW cell proliferation; cell migration; cell differentiation;  
 KW mitogenic factor; survival factor; cytotoxic factor;  
 KW differentiation factor; neurotrophic factor; hormone; cell receptor;  
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.

XX OS Homo sapiens.

XX PN WO2003072035-A2.

XX PD 04-SEP-2003.

XX PP 21-FEB-2003; 2003WO-US005241.

XX PR 22-FEB-2002; 2002US-0359461P.

XX PA (GETH ) GENENTECH INC.

XX PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;

XX PI Williams FW, Wood WI, Wu TD;

XX DR WPI; 2003-721702/68.

XX DR N-PSDB; ADP76856.

XX New PRO polypeptides, useful for diagnosing and treating an immune  
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or  
 PT diabetes mellitus.

XX Claim 10; SEQ ID NO 532; 918pp; English.

XX This invention relates to novel nucleic acids encoding human PRO secreted  
 CC and transmembrane proteins. Extracellular proteins play important roles  
 CC in the formation, differentiation and maintenance of multicellular  
 CC organisms. The fate of many individual cells (for example proliferation,  
 CC migration or differentiation) is typically governed by information  
 CC received from other cells and the immediate environment. The information  
 CC is often transmitted by secreted polypeptides (for example mitogenic  
 CC factors, survival factors, cytotoxic factors, differentiation factors,

CC neuropeptides and hormones) which are received and interpreted by diverse  
 CC cell receptors or membrane bound proteins. These membrane bound proteins  
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such  
 CC as in the blocking of receptor-ligand interactions. The current invention  
 CC provides the amino acid sequences of novel human membrane bound receptors  
 CC and proteins, along with the cDNA sequences encoding them. The novel  
 CC proteins of the invention may have cytotstatic activities through the  
 CC stimulation of chondrocytes. The nucleic acids of the invention may be  
 CC useful for the manufacture of a medicament for diagnosing or treating a  
 CC tumour in a mammal. In addition, they may be useful for measuring or  
 CC detecting the expression of a tumour associated gene. The present  
 CC sequence is the amino acid sequence of a human PRO protein of the  
 CC invention.

XX SQ Sequence 364 AA;  
 Query Match 99.0%; Score 99; DB 7; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 PSGQAGAAASESLFISNHAY 20  
 |||||:|||||:|||||  
 Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 6  
 ADJ68731  
 ID ADJ68731 standard; protein; 364 AA.  
 XX AC ADJ68731;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Human heat mitochondrial protein as a therapeutic target SeqIDS37.  
 XX KW Mitochondrial; human; screening assay; diabetes mellitus;  
 XX KW Huntington's disease; osteoarthritis;  
 XX KW Leber's hereditary optic neuropathy; LHON;  
 XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 XX KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
 XX KW osteopathic; ophthalmological; cytotstatic.  
 XX OS Homo sapiens.  
 XX FN WO2003087768-A2.  
 XX PD 23-OCT-2003.  
 XX PF 04-APR-2003; 2003WO-US010870.  
 XX PR 12-APR-2002; 2002US-0372843P.  
 XX PR 17-JUN-2002; 2002US-0389987P.  
 XX PR 20-SEP-2002; 2002US-0412418P.  
 XX (MITO-) MITOKOR.  
 XX PA (BUCK-) BUCK INST AGE RES.  
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
 XX PI Warnock DE;  
 XX DR WPI; 2003-845369/78.  
 XX PT Identifying a mitochondrial target for drug screening assays and for  
 XX PT treating diseases associated with altered mitochondrial function,  
 XX PT comprises detecting a modified polypeptide in a sample and correlating  
 XX PT with the disease.  
 XX FS Claim 1; SEQ ID NO 537; 180pp; English.  
 XX This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nootropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytotstatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.

XX SQ Sequence 364 AA;  
 Query Match 99.0%; Score 99; DB 7; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 PSGQAGAAASESLFISNHAY 20  
 |||||:|||||:|||||  
 Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 7  
 ADE77178  
 ID ADE77178 standard; protein; 364 AA.  
 XX AC ADE77178;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human protein expressed in a liver disorder #87.  
 XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;  
 XX KW tumour; liver; inflammatory disorder; immune response disorder;  
 XX KW high-throughput screening; differential gene expression; gene therapy.  
 XX OS Homo sapiens.  
 XX FN US2003108871-A1.  
 XX PD 12-JUN-2003.  
 XX PF 30-JUL-2001; 2001US-00919039.  
 XX PR 28-JUL-2000; 2000US-0222113P.  
 XX (KASE/) KASER M R.  
 XX PI Kaser MR;  
 XX DR WPI; 2004-031227/03.  
 XX DR N-PSDB; ADE77177.  
 XX PT Composition comprising several cDNAs that are differentially expressed in  
 XX PT treated human C3A liver cell cultures, useful for treating liver  
 XX PT disorders.  
 XX FS Claim 1; SEQ ID NO 343; 41pp; English.  
 XX The invention relates to a composition comprising several cDNAs that are  
 XX differentially expressed in a liver disorder. The composition is useful  
 XX for treating liver disorder such as hyperlipidaemia, hypertension, type  
 XX II diabetes, tumours of the liver and disorders of the inflammatory and  
 XX immune response. The composition is useful for a high-throughput method  
 XX of screening several molecules or compounds to identify a ligand which  
 XX specifically binds a cDNA. A protein encoded by the cDNA is useful for a  
 XX high-throughput method for using a protein to screen several molecules or  
 XX compounds to identify at least one ligand which specifically binds the  
 XX protein which involves combining the protein encoded by the cDNA with  
 XX several of molecules or compounds under conditions to allow specific  
 XX binding, and detecting specific binding between the protein and a

CC molecule or compound, therefore identifying a ligand which specifically  
 CC binds the protein. The composition is useful for detecting and  
 CC quantifying differential gene expression, can be used in gene therapy, to  
 CC formulate prognosis and to design a treatment regimen and to monitor the  
 CC efficacy of treatment. The present sequence represents the amino acid  
 CC sequence of a protein encoded by a cDNA differentially expressed in a  
 CC liver disorder.  
 XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20  
 |||||:|||||:  
 DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 8

AD102918  
 ID AD102918 standard; protein; 364 AA.

AC AD102918;

DT 22-APR-2004 (first entry)

DE Human fructose-bisphosphate aldolase.

KW gene database preparation; cDNA microarray; human;

KX fructose-bisphosphate aldolase; GP2; enzyme.

OS Homo sapiens.

PN JP2004005319-A.

PD 08-JAN-2004.

PF 10-JUN-2002; 2002JP-00168894.

PR 24-APR-2002; 2002JP-00123176.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA (KOKU-) KOKURITSU SHISHIN SHINKAI CENT SOCHO.

XX WPI; 2004-113174/12.

DR N-PSDB; AD102917.

PT Gene database production method for microarray preparation, comprises  
 PT searching homology of a candidate sequence determined by a primer probe  
 PT designing unit, for a matching candidate sequence.

PS Disclosure; Fig 9; 33pp; Japanese.

XX The invention relates to a method for preparing a gene database. The  
 CC method comprises a search unit searching homology of a candidate sequence  
 CC determined by a primer probe designing unit, for determining homologous  
 CC presence or absence of a determined candidate sequence. The method of the  
 CC invention is useful for the preparation of a microarray, such as a cDNA  
 CC microarray. The present amino acid sequence represents a human fructose-  
 CC bisphosphate aldolase.  
 XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20  
 |||||:|||||:  
 DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 9

ADQ76754

ID ADQ76754 standard; protein; 364 AA.

AC ADQ76754;

DT 07-OCT-2004 (first entry)

DE Human fructose bisphosphate aldolase A, target for anti-HIV agent.

KW Human; fructose bisphosphate aldolase A; enzyme;

KX human immunodeficiency virus; HIV; anti-HIV; virucide.

OS Homo sapiens.

PN WO2004061088-A2.

PD 22-JUL-2004.

PF 30-DEC-2003; 2003WO-US041790.

PR 30-DEC-2002; 2002US-0436936P.

PA (PPDP-) PPD DEV LP.

XX Dunn SJ;

PI WPI; 2004-534379/51.

DR N-PSDB; ADQ76753.

XX Use of an inhibitor of a member of a biological pathway for inhibiting,  
 PT suppressing, treating, or preventing human immunodeficiency virus (HIV)  
 PT infection.

Claim 1; SEQ ID NO 22; 143pp; English.

XX The present sequence is that of human fructose bisphosphate aldolase A  
 CC (ALDOA), which has been identified as a cellular target for HIV  
 CC inhibition. The invention relates to methods for identifying human  
 CC cellular genes that encode products that are necessary for productive HIV  
 CC infection for use as targets in the design of therapeutic agents for  
 CC suppressing HIV infection. The invention also includes methods for  
 CC identifying biological pathways comprising the products of such cellular  
 CC genes, as well as substrates and metabolic products of these pathways,  
 CC and methods for identifying additional human cellular genes that encode  
 CC products comprising other members of such pathways for use as targets in  
 CC the design of therapeutic agents for suppressing HIV infection. It also  
 CC relates to methods for identifying protective compounds that inhibit HIV  
 CC infection and to the use of such compounds in the treatment or prevention  
 CC of HIV. The compounds include chemical compounds such as small molecule  
 CC inhibitors or substrate compounds such as products of chemical  
 CC combinatorial libraries, or biological compounds including peptides,  
 CC antisense molecules and antibodies. In one embodiment of the invention,  
 CC the target gene encodes a target product that is a member of the  
 CC glycolysis pathway of the host cell. Random fragment expression libraries  
 CC were constructed from mRNA isolated from HL-60 and HeLa cells, and from  
 CC phytohemagglutinin-stimulated peripheral blood mononuclear cells (PBMC).  
 CC These were used for the isolation and identification of human cell-  
 CC derived genetic suppressor elements (GSEs) exhibiting HIV suppressive  
 CC activity. The human cellular genes from which these GSEs were derived  
 CC were identified, and included the ALDOA gene from a PBMC library.  
 XX

SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFVSNHAY 20  
 |||||:|||||:  
 DB 345 PSGQAGAAASESLFVSNHAY 364

RESULT 10  
ABM81754  
ID ABM81754 standard; protein; 364 AA.  
XX AC ABM81754;  
XX DT 18-NOV-2004 (first entry)  
XX DE Tumour-associated antigenic target (TAT) polypeptide PRO69617, SEQ:4521.  
XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
XX KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
XX KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
XX KW central nervous system cancer; bladder cancer; pancreatic cancer;  
XX KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
XX KW chromosome identification; chromosome mapping; gene mapping;  
XX KW gene therapy; cytostatic.  
XX OS Homo sapiens.  
XX FN WO2004030615-A2.  
XX PD 15-APR-2004.  
XX PF 29-SEP-2003; 2003WO-US028547.  
XX PR 02-OCT-2002; 2002US-0414971P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Wu TD, Zhang Z, Zhou Y;  
XX WPI; 2004-347921/32.  
XX DR N-PSDB; ACN40010.  
XX PT New tumor-associated antigenic target polypeptides and nucleic acids,  
XX PT useful in preparing a medicament for treating or detecting a  
XX PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
XX PT prostate cancer or tumor.  
XX PS Claim 12; SEQ ID NO 4521; 7273pp; English.  
XX CC The invention relates to human tumour-associated antigenic target (TAT)  
XX CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
XX CC overexpressed in cancer tissues compared to normal tissues, and may thus  
XX CC serve as effective targets for the diagnosis and treatment of cancer in  
XX CC mammals. The invention also relates to nucleic acid and polypeptide  
XX CC sequences at least 80% identical to the TAT nucleic acids and  
XX CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
XX CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
XX CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
XX CC TAT polypeptide; and methods and compositions for the treatment or  
XX CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
XX CC antibodies, antagonists, binding molecules and compositions are useful  
XX CC for diagnosing or treating a cell proliferative disorder associated with  
XX CC increased TAT expression, particularly cancers such as breast cancer,  
XX CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
XX CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
XX CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
XX CC used as hybridisation probes, in chromosome and gene mapping, in  
XX CC chromosome identification and in gene therapy. The present sequence  
XX CC represents a TAT polypeptide of the invention  
XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;  
Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 PSQGAGAAASESLFISNHAY 20  
Db 345 PSQGAGAAASESLFVSNHAY 364

RESULT 11  
ADU46860  
ID ADU46860 standard; protein; 364 AA.  
XX AC ADU46860;  
XX DT 27-JAN-2005 (first entry)  
XX DE Aldolase A fructose biphosphate.  
XX KW mammal; breast; cancer; increased risk; prognosis; biomarker.  
XX OS Homo sapiens.  
XX FN WO2004097030-A2.  
XX PD 11-NOV-2004.  
XX PF 28-APR-2004; 2004WO-US013076.  
XX PR 28-APR-2003; 2003US-0466084P.  
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX PA (KARO-) KAROLINSKA INNOVATIONS AB.  
XX PI Bergh J, Pawitan Y, Hall P, Amler LC, Han X, Huang P, Shaw P;  
XX WPI; 2004-804769/79.  
XX DR N-PSDB; ADU46827.  
XX DR GENBANK; NP\_000025.  
XX PT Identifying a mammal at increased risk for developing breast cancer by  
XX PT correlating the level of at least one biomarker with a baseline level and  
XX PT identifying a mammal at increased risk for developing breast cancer based  
XX PT on the correlation.  
XX PS Claim 1; SEQ ID NO 50; 150pp; English.  
XX CC This sequence represents the aldolase A fructose biphosphate. This  
XX CC sequence may be used in the method of the invention for identifying a  
XX CC mammal at increased risk for developing breast cancer. The method  
XX CC comprises correlating the level of at least one biomarker with a baseline  
XX CC level and identifying a mammal at increased risk for developing breast  
XX CC cancer based on the correlation. The method is useful for identifying a  
XX CC mammal at increased risk for developing breast cancer. Preferably, it is  
XX CC useful for prognosing breast cancer in a mammal and for identifying  
XX CC breast cancer in a mammal, by measuring the level of a biomarker such as  
XX CC a protein or an mRNA transcript of the biomarker.  
XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 8; Length 364;  
Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 PSQGAGAAASESLFISNHAY 20  
Db 345 PSQGAGAAASESLFVSNHAY 364

RESULT 12  
ADX05876  
ID ADX05876 standard; protein; 364 AA.  
XX AC ADX05876;  
XX DT 21-APR-2005 (first entry)  
XX DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 441.  
XX KW cytostatic; cyclin-dependent kinase; cdk; biomarker.



```

OS Homo sapiens.
XX WO2005012875-A2.
XX PD 10-FEB-2005.
XX PF 29-JUL-2004; 2004WO-US024424.
XX PR 29-JUL-2003; 2003US-0490890P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX WPI; 2005-163068/17.
XX DR N-PSDB; ADX05875.
XX PS Biomarkers useful for predicting or determining the response of a mammal
XX PT to a cancer treatment comprising administration of a modulator of cyclin-
XX PT dependent kinase activity.
XX PS Claim 5; SEQ ID NO 441; 141pp; English.
XX CC This invention describes a novel method of predicting or determining
XX CC whether a mammal will respond or is responding to an anti-cancer agent
XX CC that modulates cyclin-dependent kinase (cdk) activity. The method
XX CC comprises measuring the level of one or more biomarkers selected from
XX CC 27/4 biomarkers given in the specification (nucleotide sequence SEQ ID
XX CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
XX CC invention is utilized in a kit for determining or predicting whether
XX CC patient would be susceptible or resistant to treatment by an agent
XX CC modulating cdk activity. The invention also describes a method for
XX CC utilizing individualized genetic profiles for treating diseases and
XX CC disorders based on patient's response and molecular level, specialized
XX CC microarrays comprising the biomarkers described, antibodies directed
XX CC against the biomarkers and a cell culture model to identify biomarkers.
XX CC The cdk modulator is preferably N-5-[(5-[(1,1-Dimethylethyl)-2-
XX CC oxazolyl]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
XX CC tartaric acid salt. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
XX CC sequence represents a biomarker used in the method of the invention.
XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 9; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSCGAGAAASLSLFINHAY 20
Db 345 PSCGAGAAASLSLFINHAY 364

RESULT 13
ADZ70640
ID ADZ70640 standard; protein; 364 AA.
XX AC ADZ70640;
XX DT 30-JUN-2005 (first entry)
XX DE Human protein from lung cancer marker gene ALDOA, SEQ ID 325.
XX KW Tumor marker; lung tumor; cytostatic; neoplasm; expression;
XX KW DNA microarray.
XX OS Homo sapiens.
XX PN WO2005032495-A2.
XX PF 14-APR-2005.
XX PR 03-OCT-2003; 2003US-0508355P.

01-OCT-2004; 2004WO-US034163.
03-OCT-2003; 2003US-0508355P.
(PARB ) BAYER PHARM CORP.
Taylor I, Pauloski NR, Bigwood D;
WPI; 2005-285325/29.
N-PSDB; ADZ70639.
Providing a patient diagnosis for lung cancer comprises comparing the
level of expression of genes or gene products in a biological sample from
the patient with that from a normal individual.
Claim 3; SEQ ID NO 325; 60pp; English.
The invention relates to providing a patient diagnosis for lung cancer
comprising comparing the level of expression of genes or gene products in
a biological sample from the patient with the level of expression of
genes or gene products in a biological sample from a normal individual.
Also included are distinguishing between normal and disease tissues,
monitoring the response of a patient being treated for lung cancer by
administering an anti-cancer agent, identifying a compound useful for the
treatment of lung cancer and an array for distinguishing between normal
and disease tissues (comprising 2 or more probes corresponding to 2 or
more genes selected from any of the 200 nucleotide sequences given in the
specification, or 2 or more polypeptides comprising any of the 200 amino
acid sequences given in the specification). In providing a patient
diagnosis for lung cancer, one or more genes are selected from any of the
200 nucleotide sequences as mentioned in the specification, or one or
more gene products are polypeptides selected from any of the 20 amino
acid sequences mentioned in the specification. The methods are useful for
detecting and treating lung cancer. These may also be used for designing,
identifying and optimizing therapeutics for cancer. The present sequence
represents a protein from one of the 200 lung cancer marker genes. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
Sequence 364 AA;

Query Match 99.0%; Score 99; DB 9; Length 364;
Best Local Similarity 95.0%; Pred. No. 4.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSCGAGAAASLSLFINHAY 20
Db 345 PSCGAGAAASLSLFINHAY 364

RESULT 14
ADZ70327
ID ADZ70327 standard; protein; 364 AA.
XX AC ADZ70327;
XX DT 30-JUN-2005 (first entry)
XX DE Human protein from lung cancer marker gene ALDOA, SEQ ID 12.
XX KW Tumor marker; lung tumor; cytostatic; neoplasm; expression;
XX KW DNA microarray.
XX OS Homo sapiens.
XX PN WO2005032495-A2.
XX PF 14-APR-2005.
XX PR 01-OCT-2004; 2004WO-US034163.
XX PR 03-OCT-2003; 2003US-0508355P.

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XX (FARB ) BAYER PHARM CORP.  
 XX Taylor I, Pauloski NR, Bigwood D;  
 PI WPI; 2005-285325/29.  
 XX N-PSDB; ADZ70326.  
 DR Providing a patient diagnosis for lung cancer comprises comparing the  
 PT level of expression of genes or gene products in a biological sample from  
 PT the patient with that from a normal individual.  
 XX  
 XX Claim 3; SEQ ID NO 12; 60pp; English.  
 XX The invention relates to providing a patient diagnosis for lung cancer  
 CC comprising comparing the level of expression of genes or gene products in  
 CC a biological sample from the patient with the level of expression of  
 CC genes or gene products in a biological sample from a normal individual.  
 CC Also included are distinguishing between normal and disease tissues,  
 CC monitoring the response of a patient being treated for lung cancer by  
 CC administering an anti-cancer agent, identifying a compound useful for the  
 CC treatment of lung cancer and an array for distinguishing between normal  
 CC and disease tissues (comprising 2 or more probes corresponding to 2 or  
 CC more genes selected from any of the 200 nucleotide sequences given in the  
 CC specification, or 2 or more polypeptides comprising any of the 200 amino  
 CC acid sequences given in the specification). In providing a patient  
 CC diagnosis for lung cancer, one or more genes are selected from any of the  
 CC 200 nucleotide sequences as mentioned in the specification, or one or  
 CC more gene products are polypeptides selected from any of the 20 amino  
 CC acid sequences mentioned in the specification. The methods are useful for  
 CC detecting and treating lung cancer. These may also be used for designing,  
 CC identifying and optimizing therapeutics for cancer. The present sequence  
 CC represents a protein from one of the 200 lung cancer marker genes. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX SQ Sequence 364 AA;

Query Match 99.0%; Score 99; DB 9; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 4.2e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20  
 |||||  
 Db 345 PSGQAGAAASESLFVSNHAY 364

RESULT 15  
 ADV50900  
 ID ADV50900 standard; peptide; 22 AA.  
 XX  
 XX ADV50900;  
 XX  
 XX 10-MAR-2005 (first entry)  
 XX  
 XX Murine brain-derived aldolase peptide 7.  
 DE  
 DE Beta amyloid modulator; neuroprotective; neurotropic; Alzheimers disease;  
 KW degeneration; neurological disease; aldolase.  
 XX  
 XX Mus sp.  
 OS  
 XX JP2004361227-A.  
 PN  
 XX 24-DEC-2004.  
 PD  
 XX  
 XX 04-JUN-2003; 2003JP-00159562.  
 PF  
 XX 04-JUN-2003; 2003JP-00159562.  
 PR  
 XX (KOKU-) KOKURITSU DAIGAKU HOJIN TOHOKU DAIGAKU.  
 PA  
 XX

DR WPI; 2005-044038/05.  
 XX Comprehensive identification of beta amyloid binding protein expressed in  
 PT brain, for use against Alzheimer's disease, comprises performing a  
 PT proteomic technique.  
 XX Example; Page; 26pp; Japanese.

XX The invention relates to a novel method for comprehensive identification  
 CC of a beta amyloid-binding protein, which is expressed in the brain and  
 CC has a capacity to bind with beta amyloid 40. The method comprises  
 CC performing a proteomic technique. The method of the invention  
 CC neuroprotective and neurotropic applications. The method of the invention  
 CC may be useful in screening for a compound which inhibits the interaction  
 CC between beta amyloid and a beta amyloid-binding protein. The beta amyloid  
 CC -binding protein may be useful as an effective agent against Alzheimers  
 CC disease. The current sequence is that of a murine brain-derived peptide  
 CC of the invention which binds to beta amyloid.

XX SQ Sequence 22 AA;

Query Match 97.0%; Score 97; DB 9; Length 22;  
 Best Local Similarity 95.0%; Pred. No. 3.4e-09;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20  
 |||||  
 Db 3 PSGQAGAAASESLFISNHAY 22

Search completed: February 10, 2006, 10:05:03  
 Job time : 12.8856 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 10, 2006, 10:05:19 ; Search time 2.73063 Seconds  
(without alignments)  
704.723 Million cell updates/sec  
Title: US-10-717-243-57  
Perfect score: 100  
Sequence: 1 PSQGAGAAASLSLFTSNHAY 20  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 80: \*  
1: piri: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100.0	363	1	ADHBA	fructose-bisphosph
2	99	99.0	364	1	ADHUA	fructose-bisphosph
3	97	97.0	364	1	ADMSA	fructose-bisphosph
4	97	97.0	364	1	ADRTA	fructose-bisphosph
5	95	95.0	42	2	IS1291	aldolase C - chick
6	77	77.0	364	2	JC4189	fructose-bisphosph
7	69.5	69.5	363	2	JC4188	fructose-bisphosph
8	68	68.0	364	1	ADHUC	fructose-bisphosph
9	61	61.0	365	2	T24514	hypothetical prote
10	60.5	60.5	363	2	IS1345	zebrin II - mouse
11	59.5	59.5	363	1	ADHRC	fructose-bisphosph
12	58	58.0	137	2	IS1292	aldolase A - chick
13	57	57.0	364	2	S45346	fructose-bisphosph
14	55.5	55.5	361	1	ADFP	fructose-bisphosph
15	55.5	55.5	361	2	C42263	fructose-bisphosph
16	52	52.0	366	2	T15951	fructose 1,6-bisph
17	50	50.0	364	1	ADRTB	hypothetical prote
18	48	48.0	179	2	AF0981	fructose-bisphosph
19	48	48.0	172	2	A45532	probable exported
20	47	47.0	364	2	S48810	major merozoite su
21	46	46.0	170	2	D95178	fructose-bisphosph
22	46	46.0	170	2	C98045	conserved domain p
23	46	46.0	293	2	AE1950	hypothetical prote
24	46	46.0	364	1	ADHUB	cytosine-specific
25	46	46.0	644	2	T46277	fructose-bisphosph
26	45	45.0	357	1	ADSPAC	hypothetical prote
27	45	45.0	357	2	T12416	fructose-bisphosph
28	45	45.0	364	1	ADCHB	fructose-bisphosph
29	44	44.0	627	2	T02846	dynein light chain

ALIGNMENTS

RESULT 1

ADHUA

fructose-bisphosphate aldolase (EC 4.1.2.13) A - rabbit  
N:Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 24-Apr-1984 #sequence revision 27-Nov-1985 #text change 09-Jul-2004  
C:Accession: A92444; A90059; A90305; A90060; I46474; I46475; A01103  
R:Tolan, D.R.; Amsden, A.B.; Putney, S.D.; Urdea, M.S.; Penhoet, E.E.  
J. Biol. Chem. 259, 1127-1131, 1984  
A:Title: The complete nucleotide sequence for rabbit muscle aldolase A messenger RNA.  
A:Reference number: A92444; MUID:84111505; PMID:6546378  
A:Accession: A92444  
A:Molecule type: mRNA  
A:Residues: 1-363 <TOL>  
A:Cross-references: UNIPROT:P00883; UNIPARC:UPI0000125800; GB:K02300; NID:gl164751; PIDN  
R:Lai, C.Y.; Nakai, N.; Chang, D.  
Science 183, 1204-1206, 1974  
A:Title: Amino acid sequence of rabbit muscle aldolase and the structure of the active  
A:Reference number: A94244; MUID:74094688; PMID:4812352  
A:Contents: annotation  
A:Note: the sequence reported in this paper has been revised in references A90305 and A  
R:Nakai, N.; Chang, D.; Lai, C.Y.  
Arch. Biochem. Biophys. 166, 347-357, 1975  
A:Title: Studies on the structure of rabbit muscle aldolase. Ordering of the tryptic pe  
A:Reference number: A90059; MUID:75145171; PMID:1122141  
A:Accession: A90059  
A:Molecule type: protein  
A:Residues: 1-33,'Q',35-164 <NAK>  
A:Cross-references: UNIPARC:UPI0000172P31  
R:Benfield, P.A.; Forcina, B.G.; Gibbons, I.; Perham, R.N.  
Biochem. J. 183, 429-444, 1979  
A:Title: Extended amino acid sequences around the active-site lysine residue of class-I  
A:Reference number: A90305; MUID:80109133; PMID:534504  
A:Accession: A90305  
A:Molecule type: protein  
A:Residues: 173-200 <BEN>  
A:Cross-references: UNIPARC:UPI0000172P32  
R:Lai, C.Y.  
Arch. Biochem. Biophys. 166, 358-369, 1975  
A:Title: Studies on the structure of rabbit muscle aldolase. Determination of the prima  
A:Reference number: A90060; MUID:75145172; PMID:1122142  
A:Accession: A90060  
A:Molecule type: protein  
A:Residues: 251-278,'S',274,'E',276-277,'G',279-292,'W',294,'K',296-363 <LA12>  
A:Cross-references: UNIPARC:UPI0000172P33  
R:Hartman, F.C.; Brown, J.P.  
J. Biol. Chem. 251, 3057-3062, 1976  
A:Title: Affinity labeling of a previously undetected essential lysyl residue in class I  
A:Reference number: A92191; MUID:76190154; PMID:5453  
A:Contents: annotation; active site  
R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.

probable lipoprote  
translation initia  
thioredoxin-disulf  
hypothetical prote  
prophage p11 prote  
prophage p13 prote  
prophage p12 prote  
hypothetical prote  
thioredoxin reduct  
fructose-bisphosph  
neuron-derived rec  
glutamate synthase  
neuron-derived rec  
D-ribulose-5-phosp  
hypothetical prote

Nature 302, 718-721, 1983  
 A>Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by shc  
 A:Reference number: 146471; MUID:83167564; PMID:6687628  
 A:Accession: 146474  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 37-55 <PUT>  
 A:Cross-references: UNIPARC:UPI000016C530; EMBL:V00876; NID:g1444; PIDN:CAA24245.1; PID:  
 A:Accession: 146475  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 349-352, 'R', 354-363 <PUT>  
 A:Cross-references: UNIPARC:UPI000016C531; EMBL:V00877; NID:g1446; PIDN:CAA24246.1; PID:  
 C:Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, a  
 C:Superfamily: fructose-bisphosphate aldolase  
 C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pe  
 F:2-363/Product: fructose-bisphosphate aldolase A #status predicted <MAT>  
 F:146,229,363/Active site: Lys, Lys, Tyr #status predicted

Query Match 100.0%; Score 100; DB 1; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20  
 |||||  
 Db 344 PSQGAGAAASESLFISNHAY 363

RESULT 2  
 ADHUA  
 fructose-bisphosphate aldolase (EC 4.1.2.13) A [validated] - human  
 N:Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004  
 C:Accession: S14084; S27186; S01014; S00290; S02338; A05177; S03874; S23919; I39429; I39  
 R:Mukai, T.; Arai, Y.; Yasui, H.; Joh, K.; Hori, K.  
 Eur. J. Biochem. 195, 781-787, 1991  
 A>Title: An additional promoter functions in the human aldolase A gene, but not in rat.  
 A:Reference number: S14084; MUID:91153319; PMID:1999195  
 A:Accession: S14084  
 A:Molecule type: DNA  
 A:Residues: 1-364 <MK>  
 A:Cross-references: UNIPROT:P04075; UNIPARC:UPI00000000C5D  
 Rizzo, P.; Costanzo, P.; Lupo, A.; Ripa, E.; Borghese, A.M.; Paoletta, G.; Salvatore,  
 Eur. J. Biochem. 164, 9-13, 1987  
 A>Title: A new human species of aldolase A mRNA from fibroblasts.  
 A:Reference number: A27186; MUID:87161904; PMID:3030757  
 A:Accession: A27186  
 A:Molecule type: mRNA  
 A:Residues: 1-364 <IZZ>  
 A:Cross-references: UNIPARC:UPI00000000C5D; GB:X05236; NID:g28596; PIDN:CAA28861.1; PID:9  
 A:Experimental source: fibroblast  
 Rizzo, P.; Costanzo, P.; Lupo, A.; Ripa, E.; Paoletta, G.; Salvatore, F.  
 Eur. J. Biochem. 174, 569-578, 1988  
 A>Title: Human aldolase A gene. Structural organization and tissue-specific expression b  
 A:Reference number: S01014; MUID:88271327; PMID:3391172  
 A:Accession: S01014  
 A:Molecule type: DNA  
 A:Residues: 1-72, 'G', 74-195, 'A', 197-229, 'N', 231-279, 'S', 281-364 <IZ2>  
 A:Cross-references: UNIPARC:UPI000016A52D; GB:X12447; NID:g28613; PIDN:CAA30979.1; PID:9  
 R:Freemont, P.S.; Dunbar, B.; Fothergill-Gilmore, L.A.  
 Biochem. J. 249, 779-788, 1988  
 A>Title: The complete amino acid sequence of human skeletal-muscle fructose-bisphosphate  
 A:Reference number: S00290; MUID:88183272; PMID:3355497  
 A:Accession: S00290  
 A:Molecule type: protein  
 A:Residues: 2-358, 'I', 360-364 <PRE>  
 A:Cross-references: UNIPARC:UPI0000172F2C  
 R:Maire, P.; Gautron, S.; Hakim, V.; Gregori, C.; Mennecier, F.; Kahn, A.  
 J. Mol. Biol. 197, 425-438, 1987  
 A>Title: Characterization of three optional promoters in the 5' region of the human aldo  
 A:Reference number: S02338; MUID:88155643; PMID:3441006  
 A:Accession: S02338

A:Molecule type: DNA  
 A:Residues: 1-108 <MAI>  
 A:Cross-references: UNIPARC:UPI000016A521; EMBL:X06352; NID:g28594; PIDN:CAA29654.1; PID:  
 R:Freemont, P.S.; Dunbar, B.; Fothergill, L.A.  
 Arch. Biochem. Biophys. 228, 342-352, 1984  
 A>Title: Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr- and o-iod  
 A:Reference number: A05177; MUID:84126818; PMID:6696436  
 A:Accession: A05177  
 A:Molecule type: protein  
 A:Residues: 2-63; 148-358 <FR2>  
 A:Cross-references: UNIPARC:UPI0000172F2D; UNIPARC:UPI0000172F2E  
 R:Sakakibara, M.; Takahashi, I.; Takasaki, Y.; Mukai, T.; Hori, K.  
 Biochim. Biophys. Acta 1007, 334-342, 1989  
 A>Title: Construction and expression of human aldolase A and B expression plasmids in Es  
 A:Reference number: S03874; MUID:89194215; PMID:26649152  
 A:Accession: S03874  
 A:Molecule type: mRNA  
 A:Residues: 1-33; 357-364 <SAK>  
 A:Cross-references: UNIPARC:UPI0000172F2F; UNIPARC:UPI0000172F30  
 R:Lee, K.N.; Maxwell, M.D.; Patterson Jr., M.K.; Birckbichler, P.J.; Conway, E.  
 Biochim. Biophys. Acta 1136, 12-16, 1992  
 A>Title: Identification of transglutaminase substrates in HT29 colon cancer cells: use o  
 A:Reference number: S23919; MUID:92353128; PMID:1353685  
 A:Accession: S23919  
 A:Molecule type: protein  
 A:Residues: 2-16 <LEE>  
 A:Cross-references: UNIPARC:UPI0000071F95  
 R:Gambin, S.J.; Davies, G.J.; Grimes, J.M.; Jackson, R.M.; Littlechild, J.A.; Watson, H.  
 J. Mol. Biol. 219, 573-576, 1991  
 A>Title: Activity and Specificity of Human Aldolases.  
 A:Reference number: A43787; MUID:91278081; PMID:2056525  
 A:Contents: annotation; active site  
 R:Sakakibara, M.; Mukai, T.; Hori, K.  
 Biochem. Biophys. Res. Commun. 131, 413-420, 1985  
 A>Title: Nucleotide sequence of a cDNA clone for human aldolase: a messenger RNA in the  
 A:Reference number: I39429; MUID:85306986; PMID:3840020  
 A:Accession: I39429  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-364 <RES>  
 A:Cross-references: UNIPARC:UPI00000000C5D; GB:M11560; NID:g178350; PIDN:AAA51690.1; PID:  
 R:Tolan, D.R.; Niclas, J.; Bruce, B.D.; Lebo, R.V.  
 Am. J. Hum. Genet. 41, 907-924, 1987  
 A>Title: Evolutionary implications of the human aldolase-A, -B, -C, and -pseudogene chr  
 A:Reference number: I39435; MUID:88046782; PMID:3674018  
 A:Accession: I39435  
 A:Molecule type: mRNA  
 A:Residues: 139-364 <TOL>  
 A:Cross-references: UNIPARC:UPI000016A52E; GB:M21190; NID:g178403; PIDN:AAA51697.1; PID:  
 C:Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, f  
 C:Genetics:  
 A:Gene: GDB:ALDOA  
 A:Cross-references: GDB:118993; OMIM:103850  
 A:Map position: 16q22.2-16q22.2  
 A:Introns: 38/1  
 C:Superfamily: fructose-bisphosphate aldolase  
 C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; p  
 F:2-364/Product: fructose-bisphosphate aldolase A #status experimental <MAT>  
 F:147,230,364/Active site: Lys, Lys, Tyr #status experimental

Query Match 99.0%; Score 99; DB 1; Length 364;  
 Best Local Similarity 95.0%; Pred. No. 2.4e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20  
 |||||  
 Db 345 PSQGAGAAASESLFISNHAY 364

RESULT 3  
 ADMSA  
 fructose-bisphosphate aldolase (EC 4.1.2.13) A - mouse  
 N:Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A

C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S06323; B25388; A37062  
R:Mestek, A.; Stauffer, J.; Tolan, D.R.; Ciejek-Baez, E.  
J. Mol. Biol. 156, 229-235, 1986  
Nucleic Acids Res. 15, 10595, 1987  
A:Title: Sequence of a mouse brain aldolase A cDNA.  
A:Reference number: S06323; MUID:88096598; PMID:3697100  
A:Accession: S06323  
A:Molecule type: mRNA  
A:Residues: 1-364 <MES>  
A:Cross-references: UNIPROT:P05064; UNIPARC:UPI000000B2CC; GB:Y00516; NID:949914; PIDN:C  
A:Experimental source: brain  
R:Paolella, G.; Buono, P.; Mancini, P.P.; Izzo, P.; Salvatore, F.  
Eur. J. Biochem. 156, 229-235, 1986  
A:Title: Structure and expression of mouse aldolase genes. Brain-specific aldolase C and  
A:Reference number: A91165; MUID:86192445; PMID:3009179  
A:Accession: B25388  
A:Molecule type: mRNA  
A:Residues: 99-280, 'C', 282-355 <PAO>  
A:Cross-references: UNIPARC:UPI000016CBFC; GB:X03797; NID:949916; PIDN:CAA27423.1; PID:9  
A:Experimental source: brain  
R:Stauffer, J.K.; Colbert, M.C.; Ciejek-Baez, E.  
J. Biol. Chem. 265, 11773-11782, 1990  
A:Title: Nonconservative utilization of aldolase A alternative promoters.  
A:Reference number: A37062; MUID:90307699; PMID:2365699  
A:Accession: A37062  
A:Molecule type: DNA  
A:Residues: 1-266; 295-364 <STA>  
A:Cross-references: UNIPARC:UPI0000172F34; UNIPARC:UPI0000172F35; GB:J05517  
A:Experimental source: strain RIII S/J  
C:Superfamily: fructose-bisphosphate aldolase  
C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pe  
P:2-364/Product: fructose-bisphosphate aldolase A #status predicted <MAT>  
P:147,230,364/Active site: Lys, Lys, Tyr #status predicted  
Query Match 97.0%; Score 97; DB 1; Length 364;  
Best Local Similarity 95.0%; Pred. No. 5.2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 PSQAGAGAAASLSLFTSNHAY 20  
DB 345 PSQAGAGAAASLSLFTSNHAY 364  
RESULT 4  
ADRTA  
fructose-bisphosphate aldolase (EC 4.1.2.13) A - rat  
N:Alternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 31-Dec-2004  
C:Accession: A24532; A25383; I53307; I56408  
R:Joh, K.; Mukai, T.; Yatsuki, H.; Hori, K.  
Gene 39, 17-24, 1985  
A:Title: Rat aldolase A messenger RNA: the nucleotide sequence and multiple mRNA species  
A:Reference number: A24532; MUID:86083188; PMID:2416636  
A:Accession: A24532  
A:Molecule type: mRNA  
A:Residues: 1-364 <JOH>  
A:Cross-references: UNIPROT:P05065; UNIPROT:Q63038; UNIPARC:UPI0000170873; GB:M14420; NI  
R:Mukai, T.; Joh, K.; Arai, Y.; Yatsuki, H.; Hori, K.  
J. Biol. Chem. 261, 3347-3354, 1986  
A:Title: Tissue-specific expression of rat aldolase A mRNAs: three molecular species dif  
A:Reference number: A25383; MUID:86140113; PMID:3753977  
A:Accession: A25383  
A:Molecule type: mRNA  
A:Residues: 1-144, 'P', 146-164, 'M', 166-364 <MUK>  
A:Cross-references: UNIPARC:UPI0000167983; GB:M12919; NID:9202834; PIDN:AAA40714.1; PID:  
R:Tautsuni, R.; Tautsuni, K.  
Eur. J. Biochem. 142, 161-164, 1984  
A:Title: Two different aldolase A mRNA species in rat tissues.  
A:Reference number: I53307; MUID:84261525; PMID:6086339  
A:Accession: I53307  
A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA  
A:Residues: 324-329, 'Q', 331-356 <RES>  
A:Cross-references: UNIPARC:UPI00000E7075; GB:M28282; NID:9202849; PIDN:AAA40720.1; PID:  
R:Joh, K.; Arai, Y.; Mukai, T.; Hori, K.  
J. Mol. Biol. 190, 401-410, 1986  
A:Title: Expression of three mRNA species from a single rat aldolase A gene, differing i  
A:Reference number: I56408; MUID:87060996; PMID:3783705  
A:Accession: I56408  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-108 <RE2>  
A:Cross-references: UNIPARC:UPI0000172F36; EMBL:X04261; NID:955639; PIDN:CRAA27815.1; PI  
C:Genetics:  
A:Introns: 38/1  
C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; p  
P:2-364/Product: fructose-bisphosphate aldolase A #status predicted <MAT>  
P:147,230,364/Active site: Lys, Lys, Tyr #status predicted  
Query Match 97.0%; Score 97; DB 1; Length 364;  
Best Local Similarity 95.0%; Pred. No. 5.2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 PSQAGAGAAASLSLFTSNHAY 20  
DB 345 PSQAGAGAAASLSLFTSNHAY 364  
RESULT 5  
I51291  
aldolase C - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: I51291  
R:Meighan-Mantha, R.L.; Tolan, D.R.  
J. Cell. Biochem. 57, 423-431, 1995  
A:Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and  
A:Reference number: I51291; MUID:95286677; PMID:7768978  
A:Accession: I51291  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-42 <MEI>  
A:Cross-references: UNIPROT:Q92007; UNIPARC:UPI000000FDF44; GB:S78288; NID:9999389; PIDN  
C:Superfamily: fructose-bisphosphate aldolase  
Query Match 95.0%; Score 95; DB 2; Length 42;  
Best Local Similarity 95.0%; Pred. No. 1e-08;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 PSQAGAGAAASLSLFTSNHAY 20  
DB 23 PSQAGAGAAASLSLFTSNHAY 42  
RESULT 6  
JC4189  
fructose-bisphosphate aldolase (EC 4.1.2.13), non-muscle-type - Pacific lamprey  
N:Alternate names: non-muscle-type aldolase  
C:Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)  
C:Date: 27-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 20-Jun-2000  
C:Accession: JC4189  
R:Zhang, R.; Yatsuki, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Imai, T.; Yoshida, M.; H  
J. Biochem. 117, 545-553, 1995  
A:Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of la  
A:Reference number: JC4188; MUID:95355304; PMID:7629020  
A:Accession: JC4189  
A:Molecule type: mRNA  
A:Residues: 1-364 <ZHA>  
A:Cross-references: UNIPARC:UPI00001257F9; DBSJ:D38619; NID:91619826; PIDN:BA07607.1; P  
C:Comment: This is a glycolytic enzyme that catalyzes the reversible cleavage of fructos  
C:Superfamily: fructose-bisphosphate aldolase  
C:Keywords: aldehyde-lyase; carbon-carbon lyase; muscle  
P:230/Active site: Lys #status predicted

Query Match 77.0%; Score 77; DB 2; Length 364;  
 Best Local Similarity 70.0%; Pred. No. 9.4e-05; Mismatches 2; Indels 0; Gaps 0;  
 Matches 14; Conservative 4

QY 1 PSQAGAAASESLFISNHAY 20  
 ||:|||||:|||||  
 DB 345 PAGSGSAAASESLFIANHAY 364

RESULT 7  
 JC4188  
 fructose-bisphosphate aldolase (EC 4.1.2.13), muscle-type - Pacific lamprey  
 N:Alternate names: muscle-type aldolase  
 C:Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)  
 C:Date: 27-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 20-Jun-2000  
 C:Accession: JC4188  
 R:Zhang, R.; Yateuki, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Yoshida, M.; Horiuchi, J. Biochem. 117, 545-553, 1995  
 A:Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of lampetra tridentata  
 A:Reference number: JC4188; MUID:95355304; PMID:7629020  
 A:Accession: JC4188  
 A:Molecule type: mRNA  
 A:Residues: 1-363 <ZHA>  
 A:Cross-references: UNIPARC:UPI00001257EP; DDBJ:D38620; NID:G1619827; PIDN:BAA07608.1; EMBL:D38620  
 C:Comment: This is a glycolytic enzyme that catalyzes the reversible cleavage of fructose-1,6-bisphosphate into fructose-6-phosphate and dihydroxyacetone phosphate  
 C:Superfamily: fructose-bisphosphate aldolase  
 C:Keywords: aldehyde-lyase; carbon-carbon lyase; muscle  
 F:230/Active site: Lys #status predicted

Query Match 69.5%; Score 69.5; DB 2; Length 363;  
 Best Local Similarity 70.0%; Pred. No. 0.0016; Mismatches 3; Indels 1; Gaps 1;  
 Matches 14; Conservative 3

QY 1 PSQAGAAASESLFISNHAY 20  
 ||:|||||:|||||  
 DB 345 PTG-TGAAGESLFIANHAY 363

RESULT 8  
 ADHUC  
 fructose-bisphosphate aldolase (EC 4.1.2.13) C - human  
 N:Alternate names: aldolase C; fructose-1,6-bisphosphate triosephosphate-lyase C  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
 C:Accession: A25861; S00863; S13192  
 R:Kottmann, W.H.; Deselms, K.R.; Niclas, J.; Camerato, T.; Holman, P.S.; Green, C.J.; Tschopp, R. Biochem. 192, 805-811, 1990  
 A:Title: The complete amino acid sequence of the human aldolase C isozyme derived from a cDNA clone  
 A:Reference number: A25861; MUID:87185595; PMID:3105602  
 A:Accession: A25861  
 A:Molecule type: DNA  
 A:Residues: 1-364 <ROT>  
 A:Cross-references: UNIPROT:P09972; UNIPARC:UPI0000000C53; GB:X05196; NID:G28598; PIDN:Q05196  
 R:Buono, P.; Paoletti, G.; Mancini, P.P.; Izzo, P.; Salvatore, F.  
 Nucleic Acids Res. 16, 4733, 1988  
 A:Title: The complete nucleotide sequence of the gene coding for the human aldolase C  
 A:Reference number: S00863; MUID:88247784; PMID:3267224  
 A:Accession: S00863  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-310, 'V', 312-364 <BUO1>  
 A:Cross-references: UNIPARC:UPI000016A523; GB:X07292; NID:G28600; PIDN:CAA30270.1; PID:G28600  
 R:Buono, P.; Mancini, P.P.; Izzo, P.; Salvatore, F.  
 Eur. J. Biochem. 192, 805-811, 1990  
 A:Title: Characterization of the transcription-initiation site and of the promoter region of the human aldolase C gene  
 A:Reference number: S13192; MUID:91006178; PMID:2209624  
 A:Accession: S13192  
 A:Molecule type: DNA  
 A:Residues: 1-310, 'V', 312-364 <BUO2>  
 A:Cross-references: UNIPARC:UPI000016A523; GB:X07292; NID:G28600; PIDN:CAA30270.1; PID:G28600  
 C:Genetics:  
 A:Gene: GDB:ALDOC  
 A:Cross-references: GDB:119670; OMIM:103870

A:Map position: 17pter-17qter  
 A:Introns: 38/1; 108/3; 127/1; 180/3; 208/3; 267/1; 333/3  
 C:Superfamily: fructose-bisphosphate aldolase  
 C:Keywords: aldehyde-lyase; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; penicillin resistance  
 F:147,230,364/Active site: Lys, Lys, Tyr #status predicted

Query Match 68.0%; Score 68; DB 1; Length 364;  
 Best Local Similarity 63.2%; Pred. No. 0.0028; Mismatches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Matches 12; Conservative 5

QY 2 SQOAGAAASESLFISNHAY 20  
 ||:|||||:|||||  
 DB 346 SGEDGAAASQSLFIANHAY 364

RESULT 9  
 T24514  
 hypothetical protein T05D4.1 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T24514  
 R:McMurray, A.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19902  
 A:Accession: T24514  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-365 <WIL>  
 A:Cross-references: UNIPROT:P54216; UNIPARC:UPI0000164172; EMBL:Z81115; PIDN:CAB03291.1; EMBL:Z81115  
 A:Experimental source: clone T05D4  
 C:Genetics:  
 A:Gene: CESP:T05D4.1  
 A:Map position: 3  
 A:Introns: 32/1; 190/3  
 C:Superfamily: fructose-bisphosphate aldolase

Query Match 61.0%; Score 61; DB 2; Length 365;  
 Best Local Similarity 68.8%; Pred. No. 0.038; Mismatches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Matches 11; Conservative 4

QY 5 AGAAASESLFISNHAY 20  
 ||:|||||:|||||  
 DB 350 ADAAASQSLFIANHAY 365

RESULT 10  
 I53145  
 zebrin II - mouse  
 C:Species: Mus sp. (mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 22-Jun-1999  
 C:Accession: I53145  
 R:Ahn, A.H.; Dziennis, S.; Hawkes, R.; Herrup, K.  
 Development 120, 2081-2090, 1994  
 A:Title: The cloning of zebrin II reveals its identity with aldolase C  
 A:Reference number: I53145; MUID:95009537; PMID:7925012  
 A:Accession: I53145  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-363 <RES>  
 A:Cross-references: UNIPARC:UPI00000E5AF7; GB:S72537; NID:G619372; PIDN:AAB32064.1; PID:G619372  
 C:Superfamily: fructose-bisphosphate aldolase

Query Match 60.5%; Score 60.5; DB 2; Length 363;  
 Best Local Similarity 68.4%; Pred. No. 0.046; Mismatches 13; Conservative 3; Mismatches 2; Indels 1; Gaps 1;  
 Matches 13; Conservative 3

QY 2 SQOAGAAASESLFISNHAY 20  
 ||:|||||:|||||  
 DB 346 SGEDGAAASQSLFIANHAY 363

RESULT 11

QY 2 SQAGAAASELFISNHAY 20

F; 2-361/Product: fructose-bisphosphate al

F;2-361/Product: fructose-bisphosphate aldolase #status experimental <MAT>

F:147,230,361/Active site: Lys, Lys, Tyr #status predicted

Query Match 55.5%; Score 55.5; DB 1; Length 361;  
Best Local Similarity 63.2%; Pred. No. 0.3;  
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 SQGAGAAASESLFISNHAY 20  
: ||| | ||| : |||  
DB 344 AGSAG-AGSGSLFVANHAY 361

# RESULT 15

C42263  
fructose 1,6-bisphosphate aldolase - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: C42263  
R:Shaw-Lee, R.; Lissemore, J.L.; Sullivan, D.T.; Tolan, D.R.  
J. Biol. Chem. 267, 3959-3967, 1992  
A:Title: Alternative splicing of fructose 1,6-bisphosphate aldolase transcripts in Drosophila  
A:Reference number: A42263; MUID:92156139; PMID:1740444  
A:Accession: C42263  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-361 <SHA>  
A:Cross-references: UNIPROT:P07764; UNIPARC:UPI00001248A2; GB:M98351; GB:M76409; NID:gl5  
A>Note: sequence extracted from NCBI backbone (NCBI:82659, NCBIP:93286)  
C:Genetics:  
A:Gene: FlyBase:Ald  
A:Cross-references: FlyBase:FBgn0000064  
C:Superfamily: fructose-bisphosphate aldolase

Query Match 55.5%; Score 55.5; DB 2; Length 361;  
Best Local Similarity 63.2%; Pred. No. 0.3;  
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 SQGAGAAASESLFISNHAY 20  
: ||| | ||| : |||  
DB 344 AGSAG-AGSGSLFVANHAY 361

Search completed: February 10, 2006, 10:14:05  
Job time : 3.73063 secs



GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 16.9004 Seconds  
(without alignments)  
834.927 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQQAARSLFISFNHAY 20

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	363	1 ALDOA_RABIT	P00883 oryctolagus
2	99	99.0	260	2 Q9BWD9_HUMAN	Q9BWD9 homo sapien
3	99	99.0	363	1 ALDOA_HUMAN	P04075 homo sapien
4	99	99.0	364	2 Q6F110_HUMAN	Q6F110 homo sapien
5	99	99.0	364	2 Q5NVR5_PONPY	Q5NVR5 pongo pygma
6	97	97.0	363	1 ALDOA_MOUSE	P05064 mus musculus
7	97	97.0	363	1 ALDOA_RAT	P05065 rattus norv
8	97	97.0	364	2 Q5FWB7_MOUSE	Q5FWB7 mus musculus
9	97	97.0	364	2 Q6NY00_MOUSE	Q6NY00 mus musculus
10	95	95.0	42	2 Q92007_CHICK	Q92007 gallus gall
11	94	94.0	276	2 Q4F523_MACFA	Q4F523 macaca fasc
12	94	94.0	704	2 Q8WNT7_MACFA	Q8WNT7 macaca fasc
13	89	89.0	331	2 Q9CFQ9_MOUSE	Q9CFQ9 ambystoma m
14	88	88.0	364	2 Q9CRC1_MOUSE	Q9CRC1 mus muscu
15	88	88.0	364	2 Q6GL64_XENTR	Q6GL64 xenopus tro
16	85	85.0	364	2 Q6AY07_RAT	Q6AY07 rattus norv
17	83	83.0	364	2 Q12975_XENLA	Q12975 xenopus lae
18	83	83.0	364	2 Q76BE7_AMICA	Q76BE7 amia calva
19	82	82.0	331	2 Q76BY5_XENLA	Q76BY5 xenopus lae
20	79	79.0	279	2 Q76BF4_LEPOS	Q76BF4 lepisosteus
21	79	79.0	331	2 Q5XGT3_XENLA	Q5XGT3 xenopus lae
22	79	79.0	364	1 ALP2_LAMJA	P53446 lampetra ja
23	77	77.0	364	1 Q76B12_PROAN	Q76B12 protopetere
24	76	76.0	331	2 Q8JH72_BRARE	Q8JH72 brachydanio
25	75	75.0	364	2 Q803Q7_BRARE	Q803Q7 brachydanio
26	75	75.0	364	2 Q803Q7_BRARE	Q803Q7 brachydanio
27	74	74.0	331	2 Q76BB1_9CHON	Q76BB1 callorhinch
28	73	73.0	331	2 Q76BC5_9CHON	Q76BC5 cephaloscyll
29	72	72.0	331	2 Q76BD2_POLOR	Q76BD2 polypteru
30	72	72.0	364	2 Q6P043_BRARE	Q6P043 brachydanio
31	71	71.0	331	2 Q76BD9_ACTIBE	Q76BD9 acipenser b

32	71	71.0	331	2 Q9USF9_EPTBU	Q9USF9 eptatretus
33	70	70.0	331	2 Q76BE0_ACTIBE	Q76BE0 acipenser b
34	69.5	69.5	363	1 ALP1_LAMJA	P53445 lampetra ja
35	69	69.0	331	2 Q76BB8_9CHON	Q76BB8 brachydanio
36	69	69.0	364	2 Q7ZW73_BRARE	Q7ZW73 brachydanio
37	68	68.0	363	1 ALDOC_HUMAN	P09972 homo sapien
38	68	68.0	363	1 ALDOC_MACFA	Q9GKW3 macaca fasc
39	68	68.0	363	1 ALDOC_PANTR	Q5R1X4 pan troglod
40	68	68.0	364	2 Q5FH94_HUMAN	Q5FH94 homo sapien
41	68	68.0	364	2 Q4R4S9_MACFA	Q4R4S9 macaca fasc
42	68	68.0	394	2 Q6P0L5_HUMAN	Q6P0L5 homo sapien
43	65	65.0	331	2 Q76BC3_9CHON	Q76BC3 cephaloscyll
44	64	64.0	40	2 Q8UV41_PIG	Q8UV41 sus scrofa
45	64	64.0	330	2 Q76BF9_ORYLA	Q76BF9 oryzias lat

## ALIGNMENTS

## RESULT 1

ALDOA\_RABIT STANDARD; PRT; 363 AA.  
ID P00883; Q28671;

AC 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase).

GN Name=ALDOA;

OS Oryctolagus cuniculus (Rabbit);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

OC Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=74094688; PubMed=4812352;

RA Lai C.-Y., Nakai N., Chang D.;

RT "Amino acid sequence of rabbit muscle aldolase and the structure of

RT the active center.";

RL Science 183:1204-1206(1974).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=84111505; PubMed=6546378;

RA Tolan D.R., Amsden A.B., Putney S.D., Urdea M.S., Penhoet E.E.;

RT "The complete nucleotide sequence for rabbit muscle aldolase A

RT messenger RNA.";

RL J. Biol. Chem. 259:1127-1131(1984).

RN [3]

RP PROTEIN SEQUENCE OF 1-164.

RX MEDLINE=75145171; PubMed=1122141;

RA Nakai N., Chang D., Lai C.-Y.;

RT "Studies on the structure of rabbit muscle aldolase. Ordering of the

RT tryptic peptides; sequence of 164 amino acid residues in the NH2-

RT terminal BRN peptide.";

RL Arch. Biochem. Biophys. 166:347-357(1975).

RN [4]

RP PROTEIN SEQUENCE OF 173-200, AND SEQUENCE REVISION.

RX MEDLINE=80109133; PubMed=534504;

RA Benfield P.A., Forcina B.G., Gibbons I., Perham R.N.;

RT "Extended amino acid sequences around the active-site lysine residue

RT of class-I fructose 1,6-bisphosphate aldolases from rabbit muscle,

RT sturgeon muscle, trout muscle and ox liver.";

RL Biochem. J. 183:429-444(1979).

RN [5]

RP PROTEIN SEQUENCE OF 251-363, AND SEQUENCE REVISION.

RX MEDLINE=75145172; PubMed=1122142;

RA Lai C.-Y.;

RT "Studies on the structure of rabbit muscle aldolase. Determination of

RT the primary structure of the COOH-terminal BRN peptide; the complete

RT sequence of the subunit polypeptide chain.";

RL Arch. Biochem. Biophys. 166:358-368(1975).

RN [6]

RP NUCLEOTIDE SEQUENCE OF 37-55 AND 349-363.



FT TURN 140 141  
 FT STRAND 144 151

Query Match 100.0%; Score 100; DB 1; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20  
 |||||  
 DB 344 PSGQAGAAASESLFISNHAY 363

RESULT 2  
 Q9BWD9 HUMAN PRELIMINARY; PRT; 260 AA.

ID Q9BWD9 HUMAN  
 AC Q9BWD9; Q96B15;  
 DT 01-JUN-2001 (TREMELrel. 17, Created)  
 DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)  
 DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)  
 DE ALDOA protein (Similar to aldolase A, fructose-bisphosphate) (Fragment).  
 GN Name=ALDOA;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Paney J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- INTERACTION;  
 CC Q86WS7;-; NbExp=1; IntAct=EBI-373607, EBI-372406;  
 DR EMBL; BC000367; AAH00367.2; -; mRNA.  
 DR EMBL; BC016170; AAH16170.1; -; mRNA.  
 DR HSP; F04075; IALD.  
 DR SMR; Q9BWD9; 1-260.  
 DR IntAct; Q9BWD9; -;  
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.  
 DR GO; GO:0016829; F:lyase activity; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR InterPro; IPR000741; Aldolase\_1.  
 DR Pfam; PF00274; Glycolytic; 1.

DR ProDom; PD001128; Aldolase\_I; 1.  
 DR PROSITE; PS00158; ALDOLASE\_CLASS\_I; UNKNOWN\_1.  
 KW Glycolysis; Lyase.  
 FT NON\_TER 1  
 SQ SEQUENCE 260 AA; 27898 MW; 861B9CDE0F1P2784 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 260;  
 Best Local Similarity 95.0%; Pred. No. 8.4e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20  
 |||||  
 DB 241 PSGQAGAAASESLFISNHAY 260

RESULT 3  
 ALDOA HUMAN STANDARD; PRT; 363 AA.

ID ALDOA HUMAN  
 AC P04075; Q5FHV6;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)  
 DE (Lung cancer antigen NY-LU-1).  
 GN Name=ALDOA; Synonyms=ALDA;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;  
 RX MEDLINE=85306986; PubMed=3840020;  
 RA Sakakibara M., Mukai T., Hori K.;  
 RT "Nucleotide sequence of a cDNA clone for human aldolase: a messenger  
 RT RNA in the liver.";  
 RL Biochem. Biophys. Res. Commun. 131:413-420(1985).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Fibroblast;  
 RX MEDLINE=87161904; PubMed=3030757;  
 RA Izzo P., Costanzo P., Lupo A., Rippa E., Borghese A.M., Paoletta G.,  
 RA Salvatore F.;  
 RT "A new human species of aldolase A mRNA from fibroblasts.";  
 RL Eur. J. Biochem. 164:9-13(1987).  
 RN [3]  
 RP PROTEIN SEQUENCE.

RX MEDLINE=88183272; PubMed=3355497;  
 RA Freemont P.S., Dunbar B., Fothergill-Gilmore L.A.;  
 RT "The complete amino acid sequence of human skeletal-muscle fructose-  
 RT bisphosphate aldolase.";  
 RL Biochem. J. 249:779-788(1988).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=88271327; PubMed=3391172;  
 RA Izzo P., Costanzo P., Lupo A., Rippa E., Paoletta G., Salvatore F.;  
 RT "Human aldolase A gene. Structural organization and tissue-specific  
 RT expression by multiple promoters and alternate mRNA processing.";  
 RL Eur. J. Biochem. 174:569-578(1988).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=91153319; PubMed=1999195;  
 RA Mukai T., Arai Y., Yatsuki H., Joh K., Hori K.;  
 RT "An additional promoter functions in the human aldolase A gene, but  
 RT not in rat.";  
 RL Eur. J. Biochem. 195:781-787(1991).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RA Ebert L., Schick M., Neubert P., Schattner R., Henze S., Korn B.;  
 RT "Cloning of human full open reading frames in Gateway(TM) system entry  
 RT vector (pDONR201).";  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RN [7] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Cervix, Eye, Lung, Testis, and Uterus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratne P.H.S.,  
 RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP PROTEIN SEQUENCE OF 1-62 AND 147-357.  
 RX MEDLINE=84126818; PubMed=6696436;  
 RA Freemont P.S., Dunbar B., Fothergill L.A.;  
 RT "Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr-  
 and o-iodobenzoic acid-cleavage fragments.";  
 RL Arch. Biochem. Biophys. 228:342-352(1984).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE OF 1-107.  
 RX MEDLINE=88155643; PubMed=3441006;  
 RA Maite P., Gautron S., Hakim V., Gregori C., Mennecier F., Kahn A.;  
 RT "Characterization of three optional promoters in the 5' region of the  
 human aldolase A gene.";  
 RL J. Mol. Biol. 197:425-438(1987).  
 RN [10]  
 RP PROTEIN SEQUENCE OF 1-21.  
 RX TISSUE=Platelet;  
 RC MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;  
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J.;  
 RT "Exploring proteomes and analyzing protein processing by mass  
 spectrometric identification of sorted N-terminal peptides.";  
 RL Nat. Biotechnol. 21:566-569(2003).  
 RN [11]  
 RP NUCLEOTIDE SEQUENCE OF 138-363.  
 RX MEDLINE=88046782; PubMed=3674018;  
 RA Tolan D.R., Nicolas J., Bruce B.D., Lebo R.V.;  
 RT "Evolutionary implications of the human aldolase-A, -B, -C, and -  
 pseudogene chromosome locations.";  
 RL Am. J. Hum. Genet. 41:907-924(1987).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE=90242948; PubMed=2235208; DOI=10.1016/0014-5793(90)80211-Z;  
 RA Gambin S.J., Cooper B., Millar J.R., Davies G.J., Littlechild J.A.,  
 RA Watson H.C.;  
 RT "The crystal structure of human muscle aldolase at 3.0-A resolution.";  
 RL FEBS Lett. 262:282-286(1990).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=91278081; PubMed=2056525;  
 RA Gambin S.J., Davies G.J., Grimes J.M., Jackson R.M.,  
 RA Littlechild J.A., Watson H.C.;  
 RT "Activity and specificity of human aldolases.";  
 RL J. Mol. Biol. 219:573-576(1991).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=99156067; PubMed=10048322;  
 RA Dalby A., Dauter Z., Littlechild J.A.;  
 RT "Crystal structure of human muscle aldolase complexed with fructose

RT 1,6-bisphosphate; mechanistic implications.";  
 RL Protein Sci. 8:291-297(1999).  
 RN [15]  
 RP VARIANT HEMOLYTIC ANEMIA GLY-128.  
 RX MEDLINE=89068641; PubMed=2825199;  
 RA Kishi H., Mukai T., Hirono A., Fujii H., Miwa S., Hori K.;  
 RT "Human aldolase A deficiency associated with a hemolytic anemia:  
 thermolabile aldolase due to a single base mutation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8623-8627(1987).  
 RN [16]  
 RP VARIANT HEMOLYTIC ANEMIA GLY-128.  
 RX MEDLINE=91035340; PubMed=2229018;  
 RA Takasaki Y., Takahashi I., Mukai T., Hori K.;  
 RT "Human aldolase A of a hemolytic anemia patient with Asp-128-->Gly  
 substitution: characteristics of an enzyme generated in E. coli  
 transfected with the expression plasmid pHAAD128G.";  
 RL J. Biochem. 108:153-157(1990).  
 CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycero-  
 phosphate + D-glyceraldehyde 3-phosphate.  
 CC -1- PATHWAY: Glycolysis; sixth step.  
 CC -1- SUBUNIT: Homotetramer.  
 CC -1- DISEASE: Defects in ALDOA are a cause of hemolytic anemia  
 [MIM:103850].  
 CC -1- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous  
 glycolytic enzyme are found, aldolase A in muscle, aldolase B in  
 liver and aldolase C in brain.  
 CC -1- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase  
 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL; M11560; AAA51690.1; -; mRNA.  
 DR EMBL; X05236; CAA28861.1; -; mRNA.  
 DR EMBL; X12447; CAA30979.1; ALT\_SEQ; Genomic\_DNA.  
 DR EMBL; CR541880; CAG46678.1; -; mRNA.  
 DR EMBL; BC004333; AAH04333.1; -; mRNA.  
 DR EMBL; BC010660; AAH10660.1; -; mRNA.  
 DR EMBL; BC012880; AAH12880.1; -; mRNA.  
 DR EMBL; BC013614; AAH13614.1; -; mRNA.  
 DR EMBL; BC015888; AAH15888.1; -; mRNA.  
 DR EMBL; BC016800; AAH16800.1; -; mRNA.  
 DR EMBL; X06352; CAA29654.1; -; Genomic\_DNA.  
 DR EMBL; M21190; AAA51697.1; -; mRNA.  
 DR PIR; S14084; ADHUA.  
 DR PDB; 1ALD; X-ray; @=1-363.  
 DR PDB; 2ALD; X-ray; A=1-363.  
 DR PDB; 4ALD; X-ray; @=1-363.  
 DR SWISS-2DPAGE; P04075; HUMAN.  
 DR Aarhus/Ghent-2DPAGE; 1302; NEPHGE.  
 DR OGP; P04075; -.  
 DR Siena-2DPAGE; P04075; -.  
 DR Ensembl; ENSG00000149925; Homo sapiens.  
 DR HGNC; HGNC:414; ALDOA.  
 DR H-InvDB; HIX0012935; -.  
 DR Reactome; P04075; -.  
 DR MIM; 103850; -.  
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; TAS.  
 DR GO; GO:0006000; P:fructose metabolism; TAS.  
 DR GO; GO:0006096; P:glycolysis; TAS.  
 DR GO; GO:0006941; P:striated muscle contraction; TAS.  
 DR InterPro; IPR000741; Aldolase I.  
 DR PANTHER; PTHR11627; Aldolase I.  
 DR Pfam; PF00274; Glycolytic\_1; 1.  
 DR Prodom; PD001128; Aldolase\_1; 1.  
 DR PROSITE; PS00158; ALDOLASE\_CLASS\_I; 1.  
 KW 3D-structure; Direct protein sequencing; Disease mutation; Glycolysis;  
 KW Lyase; Multigene family; Schiff base.  
 Query Match 99.0%; Score 99; DB 1; Length 363;

```
Best Local Similarity 95.0%; Pred. No. 1.2e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
   |||||:|||||:|||||
Db 344 PSQAGAAASESLFVSNHAY 363

RESULT 4
Q6FI10 HUMAN PRELIMINARY; PRT; 364 AA.
AC Q6FI10
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fructose-bisphosphate aldolase.
GN Name=ALDOA;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR536528; CAG38765.1; -; mRNA.
DR SMR; Q6FI10; 2-364.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39420 MW; 0AAED80F755A7BE8 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
   |||||:|||||:|||||
Db 345 PSQAGAAASESLFVSNHAY 364

RESULT 5
Q5NVR5 PONY PRELIMINARY; PRT; 364 AA.
AC Q5NVR5
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fructose-bisphosphate aldolase.
GN Name=DKFPZ470J0811;
OS Pongo pygmaeus (Orangutan);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]_TaxID=9600;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR925940; CAI29598.1; -; mRNA.
DR SMR; Q5NVR5; 2-364.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
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DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Hypothetical protein; Lyase.
SQ SEQUENCE 364 AA; 39448 MW; 4DAED62BFE37CD33 CRC64;

Query Match 99.0%; Score 99; DB 2; Length 364;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFVSNHAY 20
   |||||:|||||:|||||
Db 345 PSQAGAAASESLFVSNHAY 364

RESULT 6
ALDOA MOUSE
ID ALDOA MOUSE STANDARD; PRT; 363 AA.
AC P05064;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
DE (Aldolase 1).
GN Name=Aldoa; Synonyms=Aldol;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129;
RX MEDLINE=88096598; PubMed=3697100;
RA Mestek A., Stauffer J., Tolan D.R., Ciejek-Baez E.;
RT "Sequence of a mouse brain aldolase A cDNA.";
RL Nucleic Acids Res. 15:10595-10595(1987).
RN [2]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE OF 1-265 AND 294-363.
RX MEDLINE=90307699; PubMed=2365699;
RA Stauffer J.K., Colbert M.C., Ciejek-Baez E.;
RT "Nonconservative utilization of aldolase A alternative promoters.";
RL J. Biol. Chem. 265:11773-11782(1990).
RN [4]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE OF 98-354.
RX MEDLINE=86192445; PubMed=3009179;
RA Paoletti G., Buono P., Mancini P., Izzo P., Salvatore F.;
RT "Structure and expression of mouse aldolase genes. Brain-specific
```



Db 345 PSQGGAASESLFISNHAY 364

RESULT 9

Q6NY00\_MOUSE PRELIMINARY; PRT; 364 AA.

ID Q6NY00\_MOUSE

AC Q6NY00;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 10-WAY-2005 (TREMBlrel. 30, Last annotation update)

DE Aldolase 1, A isoform.

GN Name=Aldoa;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

[1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6NCr, and C3H/He;

RC TISSUE=Hematopoietic Stem Cell, and Osteoblast;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; and

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;

RA Director MGC Project;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

[3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C3H/He; TISSUE=Osteoblast;

RA Director MGC Project;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC066801; AAH66801.1; -; mRNA.

DR EMBL; BC066218; AAH66218.1; -; mRNA.

DR HSSP; P00883; IADO.

DR SMR; Q6NY00; 2-364.

DR MGI; MGI:87994; Aldoa.

DR GO; GO:0004332; P:fructose-bisphosphate aldolase activity; IDA.

DR InterPro; IPR000741; Aldolase 1.

DR Pfam; PF00274; Glycolytic; 1.

DR ProDom; PD001128; Aldolase I; 1.

DR PROSITE; PS00158; ALDOLASE\_CLASS\_I; 1.

KW Glycolysis; Lyase.

SQ SEQUENCE 364 AA; 39312 MW; 5BD82BBE3E6D738A CRC64;

Query Match 97.0%; Score 97; DB 2; Length 364;

Best Local Similarity 95.0%; Pred. No. 2.6e-07;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 1 PSQGGAASESLFISNHAY 20

Db 345 PSQGGAASESLFISNHAY 364

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RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey CDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB169721; BAR01802.1; -, mRNA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
KW Glycolysis; Lyase.
SQ SEQUENCE 276 AA; 29587 MW; 2CDF4D877E140C2F CRC64;

Query Match          94.0%; Score 94; DB 2; Length 276;
Best Local Similarity 90.0%; Pred. No. 6e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
   ||| ||||| ||||| |||||
Db 257 PSGHAGAAASESLFVSNHAY 276

RESULT 12
Q8WNT7_MACFA
ID Q8WNT7 MACFA PRELIMINARY; PRT; 704 AA.
AC Q8WNT7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Fructose-1,6-bisphosphate aldolase A.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP TISSUE=Testis;
RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
RT in the human genome sequence.";
RL BMC Genomics 3:36-36(2002).
DR EMBL; AB066558; BAB84033.1; -, mRNA.
DR HSP; P04075; 2ALD.
DR SMR; Q8WNT7; 342-704.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
KW Glycolysis; Lyase.
SQ SEQUENCE 704 AA; 74686 MW; 02D9A004C37DFF39 CRC64;

Query Match          94.0%; Score 94; DB 2; Length 704;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
   ||| ||||| ||||| |||||
Db 695 PSGHAGAAASESLFVSNHAY 704

RESULT 13
Q76BG8_AMBME
ID Q76BG8 AMBME PRELIMINARY; PRT; 331 AA.
AC Q76BG8;

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RESULT 10
Q92007_CHICK
ID Q92007 CHICK PRELIMINARY; PRT; 42 AA.
AC Q92007;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Aldolase C (Aldolase A) (Fragment).
GN Name=aldolase C;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95286677; PubMed=7768978;
RA Meighan-Mantha R.L., Tolan D.R.;
RT "Noncoordinate changes in the steady-state mRNA expressed from
RT aldolase A and aldolase C genes during differentiation of chicken
RT myoblasts.";
RL J. Cell. Biochem. 57:423-431(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RA Meighan-Mantha R.L., Tolan D.R.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Meighan-Mantha R.L., Tolan D.R.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; S78288; AAB34479.1; -, mRNA.
DR EMBL; L25374; AAA99864.1; -, mRNA.
DR EMBL; L25373; AAA48588.1; -, mRNA.
DR PIR; I51291; I51291.
DR HSP; P00883; 6ALD.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
FT NON_TER 42
SQ SEQUENCE 42 AA; 4384 MW; 7B0E34B8C695DC4B CRC64;

Query Match          95.0%; Score 95; DB 2; Length 42;
Best Local Similarity 95.0%; Pred. No. 5.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
   ||| ||||| ||||| |||||
Db 23 PSGHAGAAASESLFISNHAY 42

RESULT 11
Q4R523_MACFA
ID Q4R523 MACFA PRELIMINARY; PRT; 276 AA.
AC Q4R523;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Brain cDNA, clone: Qf1A-11254, similar to human aldolase A, fructose-
DE bisphosphate (ALDOA), transcript variant 2,.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its

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Genome Res. 10:1757-1771(2000).  
 [6]  
 RA NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito K., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Cobley V.;  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK016845; BAB30459.1; -; mRNA.  
 DR EMBL; AK014956; BAB29638.1; -; mRNA.  
 DR EMBL; AL928642; CAI26150.1; -; Genomic\_DNA.  
 DR HSR; P04075; 2ALD.  
 DR SMR; Q9CPO9; 2-364.  
 DR Ensembl; ENSMUSG0000059343; Mus musculus.  
 DR MGI; MGI:78994; Aldoa.  
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.  
 DR InterPro; IPR000741; Aldolase I.  
 DR Pfam; PF00274; Glycolytic; 1.  
 DR ProDom; PD001128; Aldolase I; 1.  
 DR PROSITE; PS00158; ALDOLASE\_CLASS\_I; 1.  
 DR GlycoLyse; Lyase.  
 KW SEQUENCE 364 AA; 39285 MW; 53C8A3919977FF2F CRC64;  
 SQ  
 Query Match 88.0%; Score 88; DB 2; Length 364;  
 Best Local Similarity 85.0%; Pred. No. 8e-06;  
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 PSQGAGAAASESLFSINRAY 20  
 Db 345 PSQGTGATASESLFSINRAY 364  
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 ID Q9CRCL1 MOUSE PRELIMINARY; PRT; 364 AA.  
 AC Q9CRCL1  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
 DE library, clone:4933425L11 product:fructose-bisphosphate aldolase  
 DE (EC 4.1.2.13) A homolog (Mus musculus adult male testis cDNA, RIKEN  
 DE full-length enriched library, clone:1700027120 product:fructose-  
 DE bisphosphate aldolase (EC 4.1.2.13) A homolog)  
 DE Name=4933425L11R1k;  
 GN Mus musculus (Mouse)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Furuno M., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie I., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hatanaka M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

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RT *RIKEN integrated sequence analysis (RISA) system-384-format
RT Sequencing pipeline with 384 multicapillary sequencer."
RN Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK016920; BAB30498.1; -; mRNA.
DR EMBL; AK006425; BAB24582.1; -; mRNA.
DR HSSP; P04075; 2ALD.
DR SMR; Q9CRCL; 3-364.
DR Ensembl; ENSMUSG00000063129; Mus musculus.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
DR GO; GO:0016823; F:lyase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000741; Aldolase_I.
DR Pfam; PF00274; Glycolytic; 1.
DR ProDom; PD001128; Aldolase_I; 1.
DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
KW Glycolysis; Lyase.
SQ SEQUENCE 364 AA; 39370 MW; 0360CD12B8509A0D CRC64;

Query Match      88.0%; Score 88; DB 2; Length 364;
Best Local Similarity 85.0%; Pred. No. 8e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSGQAGAAASESLFISNHAY 20
Db 345 PSNESCAGAAASESLFISNHAY 364
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Job time : 17.9004 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)  
414.909 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	100	100.0	20	1	US-08-425-336-57
3	100	100.0	20	1	US-08-488-113B-57
4	100	100.0	20	1	US-08-477-484B-57
5	100	100.0	20	1	US-08-646-360-57
6	100	100.0	20	2	US-08-839-765-57
7	100	100.0	20	2	US-09-136-389-57
8	100	100.0	20	2	US-08-610-838-57
9	100	100.0	20	2	US-09-711-485-57
10	100	100.0	20	4	PCT-US92-09487-59
11	99	99.0	364	2	US-09-919-039-343
12	99	99.0	419	2	US-09-949-016-8781
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Sequence 47516, A  
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Sequence 13251, A  
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## ALIGNMENTS

### RESULT 1

US-07-988-430-59

; Sequence 59, Application US/07988430

; Patent No. 5416202

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Lane, Julie A.

; APPLICANT: Lei, Shau-Ping

; TITLE OF INVENTION: Materials Comprising and Methods of

; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/988,430

; FILING DATE: 19921209

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5416202and, Greta E.

; REGISTRATION NUMBER: 35302

; REFERENCE/DOCKET NUMBER: 31133

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-988-430-59

Query Match 100.0%; Score 100; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQGAAGAAASESLFISNHAY 20  
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Db 1 PSQGAAGAAASESLFISNHAY 20

## RESULT 2

US-08-425-336-57

; Sequence 57, Application US/08425336  
; Patent No. 5621083  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691

FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989

REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-425-336-57

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Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 PSQGAAGAAASESLFISNHAY 20

## RESULT 3

US-08-488-113B-57

; Sequence 57, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155  
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-488-113B-57

Query Match 100.0%; Score 100; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQGAAGAAASESLFISNHAY 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 PSQGAAGAAASESLFISNHAY 20

## RESULT 4

US-08-477-484B-57

; Sequence 57, Application US/08477484B  
; Patent No. 5756699  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-484B-57  
Query Match 100.0%; Score 100; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PSGQAGAAASLSLFSNHAY 20  
Db 1 PSGQAGAAASLSLFSNHAY 20  
RESULT 5  
US-08-646-360-57  
Sequence 57, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-646-360-57  
Query Match 100.0%; Score 100; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PSGQAGAAASLSLFSNHAY 20  
Db 1 PSGQAGAAASLSLFSNHAY 20  
RESULT 6  
US-08-839-765-57  
Sequence 57, Application US/08839765  
Patent No. 6146631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-839-765-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 7
US-09-136-389-57
; Sequence 57, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-136-389-57

Query Match 100.0%; Score 100; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20
Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 8
US-09-610-838-57
; Sequence 57, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
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;; FILING DATE: 18-AUG-1998  
;; APPLICATION NUMBER: 08/646,360  
;; FILING DATE: 13-MAY-1996  
;; APPLICATION NUMBER: PCT/US94/05348  
;; FILING DATE: 12-MAY-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/064,691  
;; FILING DATE: 12-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/988,430  
;; FILING DATE: 09-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 200-70.P4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 57:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-09-610-838-57

Query Match 100.0%; Score 100; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20  
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Db 1 PSGQAGAAASESLFISNHAY 20

RESULT 9  
US-09-711-485-57  
; Sequence 57, Application US/09711485  
; Patent No. 6649742  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
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; APPLICATION NUMBER: US/09/711.485  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/839,765  
; FILING DATE:  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/064,691  
;; FILING DATE: 12-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/988,430  
;; FILING DATE: 09-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 57:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-09-711-485-57

Query Match 100.0%; Score 100; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSGQAGAAASESLFISNHAY 20  
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Db 1 PSGQAGAAASESLFISNHAY 20

## RESULT 10

PCT-US92-09487-59  
; Sequence 59, Application PC/TUS9209487  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09487  
; FILING DATE: 19921104  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:

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; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US92-09487-59

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Query Match      100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 PSGQAGAAASESLFISNHAY 20

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RESULT 11
US-09-919-039-343
; Sequence 343, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 343
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 2706606CD1
US-09-919-039-343

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RESULT 12  
US-09-949-016-8781  
; Sequence 8781, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8781
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8781

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Query Match      99.0%; Score 99; DB 2; Length 419;
Best Local Similarity 95.0%; Pred. No. 1.2e-08;
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RESULT 13
US-09-976-594-390
; Sequence 390, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELLS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 390
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2705321CD1
US-09-976-594-390

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RESULT 14
US-09-583-110-3353
; Sequence 3353, Application US/09583110
; Patent No. 669703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: Nucleic Acid and
; TITLE OF INVENTION: Pneumoniae for D
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3353
; LENGTH: 170
; TYPE: PrT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3353

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Query Match 46.0%; Score 46; DB 2; Length 170;  
Best Local Similarity 52.4%; Pred. No. 4.6;  
Matches 11; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SQQAGAAASE--SLFISNHAY 20  
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Db 42 SQQAGVVCQEPADFFESNHL 62

RESULT 15  
US-09-107-433-3864  
; Sequence 3864, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 3864:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 171 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...171  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3864:  
US-09-107-433-3864

Query Match 46.0%; Score 46; DB 2; Length 171;  
Best Local Similarity 52.4%; Pred. No. 4.6;  
Matches 11; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 2 SQQAGAAASE--SLFISNHAY 20  
||||| |  
Db 43 SQQAGVVCQEPADFFESNHL 63

Search completed: February 10, 2006, 10:15:58  
Job time : 3.98524 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 13.0627 Seconds  
(without alignments)  
639.727 Million cell updates/sec

Title: US-10-717-243-57

Perfect score: 100

Sequence: 1 PSQQGAAASLSLFISNHAY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	20	4	US-10-127-890-57
2	100	100.0	20	5	US-10-717-243-57
3	99	99.0	153	4	US-10-264-049-3838
4	99	99.0	364	3	US-09-919-039-343
5	99	99.0	364	4	US-10-408-765A-537
6	99	99.0	364	5	US-10-370-715B-532
7	97	97.0	364	4	US-10-205-219-67
8	96	96.0	112	4	US-10-425-115-196160
9	95	95.0	31	3	US-09-925-301-1462
10	68	68.0	364	4	US-10-170-385-259
11	68	68.0	364	4	US-10-408-765A-98
12	61	61.0	365	4	US-10-369-493-5923
13	55.5	55.5	361	4	US-10-108-605-255
14	55.5	55.5	361	6	US-11-097-143-27699
15	52	52.0	366	4	US-10-369-493-5735
16	51	51.0	358	4	US-10-767-701-46629
17	51	51.0	361	4	US-10-425-115-269098
18	51	51.0	371	4	US-10-425-114-65982
19	51	51.0	371	4	US-10-425-115-269100
20	50.5	50.5	215	4	US-10-029-386-33867
21	50.5	50.5	836	4	US-10-108-260A-3700
22	47	47.0	1223	6	US-11-097-143-16989
23	46	46.0	98	4	US-10-424-599-161041
24	46	46.0	132	4	US-10-484-364-2
25	46	46.0	170	5	US-10-472-928-3140
26	46	46.0	171	5	US-10-617-320-3864
27	46	46.0	332	4	US-10-425-114-44042

28 46 46.0 355 4 US-10-425-114-44220 Sequence 44220, A  
29 46 46.0 355 4 US-10-425-114-45677 Sequence 45677, A  
30 46 46.0 358 4 US-10-424-599-222971 Sequence 222971, A  
31 46 46.0 364 4 US-10-177-293-8 Sequence 8, Appli  
32 46 46.0 372 4 US-10-425-114-43852 Sequence 43852, A  
33 46 46.0 372 4 US-10-425-114-44097 Sequence 44097, A  
34 46 46.0 372 4 US-10-425-114-44837 Sequence 44837, A  
35 46 46.0 375 4 US-10-425-114-45592 Sequence 45592, A  
36 46 46.0 375 4 US-10-425-114-51423 Sequence 51423, A  
37 46 46.0 375 4 US-10-425-114-55978 Sequence 55978, A  
38 46 46.0 375 4 US-10-425-114-55981 Sequence 55981, A  
39 46 46.0 392 4 US-10-437-963-151748 Sequence 151748, A  
40 46 46.0 416 4 US-10-437-963-180885 Sequence 180885, A  
41 46 46.0 644 4 US-10-408-765A-1196 Sequence 1196, Ap  
42 46 46.0 902 4 US-10-029-386-32110 Sequence 32110, A  
43 45.5 45.5 388 4 US-10-767-701-46406 Sequence 46406, A  
44 45.5 45.5 404 4 US-10-425-115-351374 Sequence 351374, A  
45 45.5 45.5 414 4 US-10-425-114-70495 Sequence 70495, A

#### ALIGNMENTS

#### RESULT 1

US-10-127-890-57

; Sequence 57, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 200-70.P4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155

; TELE: 650 388-1248

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-127-890-57

Query Match          100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
Db 1 PSQGAGAAASESLFISNHAY 20

RESULT 2
US-10-717-243-57
; Sequence 57, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-717-243-57

Query Match          100.0%; Score 100; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
Db 1 PSQGAGAAASESLFISNHAY 20

RESULT 3
US-10-264-049-3838
; Sequence 3838, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3838
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3838

Query Match          99.0%; Score 99; DB 4; Length 153;
Best Local Similarity 95.0%; Pred. No. 7.9e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
Db 134 PSQGAGAAASESLFVSNHAY 153

RESULT 4
US-09-919-039-343
; Sequence 343, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 343
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 27066060CD1
US-09-919-039-343

Query Match          99.0%; Score 99; DB 3; Length 364;
Best Local Similarity 95.0%; Pred. No. 2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQGAGAAASESLFISNHAY 20
Db 345 PSQGAGAAASESLFVSNHAY 364

RESULT 5
```

US-10-408-765A-537  
; Sequence 537, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Bojin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale B.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 537  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-408-765A-537  
Query Match 99.0%; Score 99; DB 4; Length 364;  
Best Local Similarity 95.0%; Pred. No. 2e-07;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20  
DB 345 PSGQAGAAASLSLFVSNHAY 364

## RESULT 6

US-10-370-715B-532  
; Sequence 532, Application US/10370715B  
; Publication No. US20040258678A1  
; GENERAL INFORMATION:

; APPLICANT: Bodary, Sarah C.  
; APPLICANT: Clark, Hillary  
; APPLICANT: Brisdell, Hunte  
; APPLICANT: Jackman, Janet  
; APPLICANT: Schoenfeld, Jill R.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Wu, Thomas D.  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune

; TITLE OF INVENTION: Related Diseases  
; FILE REFERENCE: P1948R1-US  
; CURRENT APPLICATION NUMBER: US/10/370,715B  
; CURRENT FILING DATE: 2003-02-21  
; NUMBER OF SEQ ID NOS: 742  
; SEQ ID NO 532  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Homo sapien

US-10-370-715B-532

Query Match 99.0%; Score 99; DB 5; Length 364;  
Best Local Similarity 95.0%; Pred. No. 2e-07;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20  
DB 345 PSGQAGAAASLSLFVSNHAY 364

## RESULT 7

US-10-205-219-67  
; Sequence 67, Application US/10205219  
; Publication No. US20030138803A1  
; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Pinnock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

; FILE REFERENCE: WL-A-018200  
; CURRENT APPLICATION NUMBER: US/10/205,219  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 67  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Aldolase A  
; US-10-205-219-67

Query Match 97.0%; Score 97; DB 4; Length 364;  
Best Local Similarity 95.0%; Pred. No. 4.3e-07;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20  
DB 345 PSGQAGAAASLSLFISNHAY 364

## RESULT 8

US-10-425-115-196160  
; Sequence 196160, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kowalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 196160  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Zea mays

; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(112)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MFT4577\_110484C.1.pep  
; US-10-425-115-196160

Query Match 96.0%; Score 96; DB 4; Length 112;  
Best Local Similarity 95.0%; Pred. No. 1.7e-07;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSGQAGAAASLSLFISNHAY 20  
DB 93 PSGQAGAAASLSLFISNHAY 112

## RESULT 9

US-09-925-301-1462  
; Sequence 1462, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

```
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1462
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1462

Query Match      95.0%; Score 95; DB 3; Length 31;
Best Local Similarity 90.0%; Pred. No. 6.1e-08;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSQAGAAASESLFISNHAY 20
Db 12 PXQAGAAASESLFVSNHAY 31

RESULT 10
US-10-170-385-259
; Sequence 259, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Mundy, Neil Raymond
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05459
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-259

Query Match      68.0%; Score 68; DB 4; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.021;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SQAGAAASESLFISNHAY 20
Db 346 SGEDGAAASQSLYIANHAY 364

RESULT 11
US-10-408-765A-98
; Sequence 98, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
```

```
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-98

Query Match      68.0%; Score 68; DB 4; Length 364;
Best Local Similarity 63.2%; Pred. No. 0.021;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 SQAGAAASESLFISNHAY 20
Db 346 SGEDGAAASQSLYIANHAY 364

RESULT 12
US-10-369-493-5923
; Sequence 5923, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5923
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5923

Query Match      61.0%; Score 61; DB 4; Length 365;
Best Local Similarity 68.8%; Pred. No. 0.28;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGAAASESLFISNHAY 20
Db 350 ADAAASQSLFVANHAY 365

RESULT 13
US-10-108-605-255
; Sequence 255, Application US/10108605
; Publication No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
```



```
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 255
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-255

Query Match          55.5%; Score 55.5; DB 4; Length 361;
Best Local Similarity 63.2%; Pred. No. 2.2;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Oy      2 SQGAGAAASESLFISNHAY 20
      :|||||:|||||:|||||
Db      344 AGSAG-AGGSLFVANHAY 361

RESULT 14
US-11-097-143-27699
; Sequence 27699, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27699
; LENGTH: 361
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-27699

Query Match          55.5%; Score 55.5; DB 6; Length 361;
Best Local Similarity 63.2%; Pred. No. 2.2;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Oy      2 SQGAGAAASESLFISNHAY 20
      :|||||:|||||:|||||
Db      344 AGSAG-AGGSLFVANHAY 361

RESULT 15
US-10-369-493-5735
; Sequence 5735, Application US/10369493
```

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; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5735
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5735

Query Match          52.0%; Score 52; DB 4; Length 366;
Best Local Similarity 56.2%; Pred. No. 8;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy      5 AGAAASESLFISNHAY 20
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Db      351 AAGAAASESLFVAKHSY 366

Search completed: February 10, 2006, 10:44:47
Job time : 14.0627 secs
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ORGANISM: ARTIFICIAL

Query Match 40.0%; Score 40; DB 6; Length 748;  
Best Local Similarity 47.4%; Pred. No. 50;  
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

## RESULT 7

US-11-115-639-38  
 ; Sequence 38, Application US/11115639  
 ; Publication No. US20050282242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothstein, David  
 ; APPLICANT: Murphy, Christopher  
 ; APPLICANT: MacNeil, Ian  
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL  
 ; FILE REFERENCE: 50150/075003  
 ; CURRENT APPLICATION NUMBER: US/11/115,639  
 ; CURRENT FILING DATE: 2005-04-27  
 ; PRIOR APPLICATION NUMBER: 60/566,858  
 ; PRIOR FILING DATE: 2004-04-30  
 ; PRIOR APPLICATION NUMBER: 60/565,679  
 ; PRIOR FILING DATE: 2004-04-27  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 38  
 ; LENGTH: 1343  
 ; TYPE: PRT  
 ; ORGANISM: H. influenzae  
 US-11-115-639-38

Query Match 38.5%; Score 38.5; DB 7; Length 1343;  
 Best Local Similarity 47.8%; Pred. No. 1.8e+02;  
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

Qy 1 PSQAG-AAASESLF--ISNHAY 20  
 Db 43 PEGQGLEAFRSVPFIVSNNGY 65

RESULT 8  
 US-11-115-639-39  
 ; Sequence 39, Application US/11115639  
 ; Publication No. US20050282242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothstein, David  
 ; APPLICANT: Murphy, Christopher  
 ; APPLICANT: MacNeil, Ian  
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL  
 ; FILE REFERENCE: 50150/075003  
 ; CURRENT APPLICATION NUMBER: US/11/115,639  
 ; CURRENT FILING DATE: 2005-04-27  
 ; PRIOR APPLICATION NUMBER: 60/566,858  
 ; PRIOR FILING DATE: 2004-04-30  
 ; PRIOR APPLICATION NUMBER: 60/565,679  
 ; PRIOR FILING DATE: 2004-04-27  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 39  
 ; LENGTH: 1343  
 ; TYPE: PRT  
 ; ORGANISM: H. influenzae  
 US-11-115-639-39

Query Match 38.5%; Score 38.5; DB 7; Length 1343;  
 Best Local Similarity 47.8%; Pred. No. 1.8e+02;  
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

Qy 1 PSQAG-AAASESLF--ISNHAY 20  
 Db 43 PEGQGLEAFRSVPFIVSNNGY 65

RESULT 9  
 US-11-115-639-40  
 ; Sequence 40, Application US/11115639  
 ; Publication No. US20050282242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothstein, David

; APPLICANT: Murphy, Christopher  
 ; APPLICANT: MacNeil, Ian  
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL  
 ; FILE REFERENCE: 50150/075003  
 ; CURRENT APPLICATION NUMBER: US/11/115,639  
 ; CURRENT FILING DATE: 2005-04-27  
 ; PRIOR APPLICATION NUMBER: 60/566,858  
 ; PRIOR FILING DATE: 2004-04-30  
 ; PRIOR APPLICATION NUMBER: 60/565,679  
 ; PRIOR FILING DATE: 2004-04-27  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 40  
 ; LENGTH: 1343  
 ; TYPE: PRT  
 ; ORGANISM: H. influenzae  
 US-11-115-639-40

Query Match 38.5%; Score 38.5; DB 7; Length 1343;  
 Best Local Similarity 47.8%; Pred. No. 1.8e+02;  
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

Qy 1 PSQAG-AAASESLF--ISNHAY 20  
 Db 43 PEGQGLEAFRSVPFIVSNNGY 65

RESULT 10  
 US-11-115-639-41  
 ; Sequence 41, Application US/11115639  
 ; Publication No. US20050282242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothstein, David  
 ; APPLICANT: Murphy, Christopher  
 ; APPLICANT: MacNeil, Ian  
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL  
 ; FILE REFERENCE: 50150/075003  
 ; CURRENT APPLICATION NUMBER: US/11/115,639  
 ; CURRENT FILING DATE: 2005-04-27  
 ; PRIOR APPLICATION NUMBER: 60/566,858  
 ; PRIOR FILING DATE: 2004-04-30  
 ; PRIOR APPLICATION NUMBER: 60/565,679  
 ; PRIOR FILING DATE: 2004-04-27  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 41  
 ; LENGTH: 1343  
 ; TYPE: PRT  
 ; ORGANISM: H. influenzae  
 US-11-115-639-41

Query Match 38.5%; Score 38.5; DB 7; Length 1343;  
 Best Local Similarity 47.8%; Pred. No. 1.8e+02;  
 Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

Qy 1 PSQAG-AAASESLF--ISNHAY 20  
 Db 43 PEGQGLEAFRSVPFIVSNNGY 65

RESULT 11  
 US-11-055-822-88  
 ; Sequence 88, Application US/11055822  
 ; Publication No. US20050260707A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompeius, Markus  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberhauer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING

<p>; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS</p> <p>; FILE REFERENCE: BGI-121CPCN</p> <p>; CURRENT APPLICATION NUMBER: US/11/055,822</p> <p>; CURRENT FILING DATE: 2005-02-11</p> <p>; PRIOR APPLICATION NUMBER: 09/606,740</p> <p>; PRIOR FILING DATE: 2000-06-23</p> <p>; PRIOR APPLICATION NUMBER: 60/141,031</p> <p>; PRIOR FILING DATE: 1999-06-25</p> <p>; PRIOR APPLICATION NUMBER: 60/142,101</p> <p>; PRIOR FILING DATE: 1999-07-02</p> <p>; PRIOR APPLICATION NUMBER: 60/148,613</p> <p>; PRIOR FILING DATE: 1999-08-12</p> <p>; PRIOR APPLICATION NUMBER: 60/187,970</p> <p>; PRIOR FILING DATE: 2000-03-09</p> <p>; PRIOR APPLICATION NUMBER: DE 19930476.9</p> <p>; PRIOR FILING DATE: 1999-07-01</p> <p>; PRIOR APPLICATION NUMBER: DE 19931415.2</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931418.7</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931419.5</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931420.9</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; Remaining Prior Application data removed - See File Wrapper or PALM.</p> <p>; NUMBER OF SEQ ID NOS: 1158</p> <p>; SEQ ID NO 88</p> <p>; LENGTH: 209</p> <p>; TYPE: PRT</p> <p>; ORGANISM: Corynebacterium glutamicum</p> <p>US-11-055-822-88</p>	<p>Query Match            38.0%;   Score 38;   DB 7;   Length 209;</p> <p>Best Local Similarity   44.4%;   Pred. No. 26;</p> <p>Matches     8;   Conservative     4;   Mismatches     6;   Indels     0;   Gaps     0;</p>	<p>QY        2   SGOAGAAASBSLFI SNHA 19</p> <p>Db        41   SGPAGLAQAQLTRAGHS 58</p>
<p>RESULT 12</p> <p>US-11-055-822-90</p> <p>; Sequence 90, Application US/11055822</p> <p>; Publication No. US20050260707A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Pompejus, Markus</p> <p>; APPLICANT: Kroger, Burkhard</p> <p>; APPLICANT: Schroder, Hartwig</p> <p>; APPLICANT: Zelder, Oskar</p> <p>; APPLICANT: Haberer, Gregor</p> <p>; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING</p> <p>; FILE REFERENCE: BGI-121CPCN</p> <p>; CURRENT APPLICATION NUMBER: US/11/055,822</p> <p>; CURRENT FILING DATE: 2005-02-11</p> <p>; PRIOR APPLICATION NUMBER: 09/606,740</p> <p>; PRIOR FILING DATE: 2000-06-23</p> <p>; PRIOR APPLICATION NUMBER: 60/141,031</p> <p>; PRIOR FILING DATE: 1999-06-25</p> <p>; PRIOR APPLICATION NUMBER: 60/142,101</p> <p>; PRIOR FILING DATE: 1999-07-02</p> <p>; PRIOR APPLICATION NUMBER: 60/148,613</p> <p>; PRIOR FILING DATE: 1999-08-12</p> <p>; PRIOR APPLICATION NUMBER: 60/187,970</p> <p>; PRIOR FILING DATE: 2000-03-09</p> <p>; PRIOR APPLICATION NUMBER: DE 19930476.9</p> <p>; PRIOR FILING DATE: 1999-07-01</p> <p>; PRIOR APPLICATION NUMBER: DE 19931415.2</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931418.7</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931419.5</p>	<p>Query Match            38.0%;   Score 38;   DB 7;   Length 209;</p> <p>Best Local Similarity   44.4%;   Pred. No. 26;</p> <p>Matches     8;   Conservative     4;   Mismatches     6;   Indels     0;   Gaps     0;</p>	<p>QY        2   SGOAGAAASBSLFI SNHA 19</p> <p>Db        41   SGPAGLAQAQLTRAGHS 58</p>
<p>US-11-055-822-90</p> <p>; Sequence 90, Application US/11055822</p> <p>; Publication No. US20050260707A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Pompejus, Markus</p> <p>; APPLICANT: Kroger, Burkhard</p> <p>; APPLICANT: Schroder, Hartwig</p> <p>; APPLICANT: Zelder, Oskar</p> <p>; APPLICANT: Haberer, Gregor</p> <p>; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING</p> <p>; FILE REFERENCE: BGI-121CPCN</p> <p>; CURRENT APPLICATION NUMBER: US/11/055,822</p> <p>; CURRENT FILING DATE: 2005-02-11</p> <p>; PRIOR APPLICATION NUMBER: 09/606,740</p> <p>; PRIOR FILING DATE: 2000-06-23</p> <p>; PRIOR APPLICATION NUMBER: 60/141,031</p> <p>; PRIOR FILING DATE: 1999-06-25</p> <p>; PRIOR APPLICATION NUMBER: 60/142,101</p> <p>; PRIOR FILING DATE: 1999-07-02</p> <p>; PRIOR APPLICATION NUMBER: 60/148,613</p> <p>; PRIOR FILING DATE: 1999-08-12</p> <p>; PRIOR APPLICATION NUMBER: 60/187,970</p> <p>; PRIOR FILING DATE: 2000-03-09</p> <p>; PRIOR APPLICATION NUMBER: DE 19930476.9</p> <p>; PRIOR FILING DATE: 1999-07-01</p> <p>; PRIOR APPLICATION NUMBER: DE 19931415.2</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931418.7</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931419.5</p>	<p>Query Match            38.0%;   Score 38;   DB 7;   Length 209;</p> <p>Best Local Similarity   44.4%;   Pred. No. 26;</p> <p>Matches     8;   Conservative     4;   Mismatches     6;   Indels     0;   Gaps     0;</p>	<p>QY        2   SGOAGAAASBSLFI SNHA 19</p> <p>Db        41   SGPAGLAQAQLTRAGHS 58</p>
<p>US-11-055-822-90</p> <p>; Sequence 90, Application US/11055822</p> <p>; Publication No. US20050260707A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Pompejus, Markus</p> <p>; APPLICANT: Kroger, Burkhard</p> <p>; APPLICANT: Schroder, Hartwig</p> <p>; APPLICANT: Zelder, Oskar</p> <p>; APPLICANT: Haberer, Gregor</p> <p>; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING</p> <p>; FILE REFERENCE: BGI-121CPCN</p> <p>; CURRENT APPLICATION NUMBER: US/11/055,822</p> <p>; CURRENT FILING DATE: 2005-02-11</p> <p>; PRIOR APPLICATION NUMBER: 09/606,740</p> <p>; PRIOR FILING DATE: 2000-06-23</p> <p>; PRIOR APPLICATION NUMBER: 60/141,031</p> <p>; PRIOR FILING DATE: 1999-06-25</p> <p>; PRIOR APPLICATION NUMBER: 60/142,101</p> <p>; PRIOR FILING DATE: 1999-07-02</p> <p>; PRIOR APPLICATION NUMBER: 60/148,613</p> <p>; PRIOR FILING DATE: 1999-08-12</p> <p>; PRIOR APPLICATION NUMBER: 60/187,970</p> <p>; PRIOR FILING DATE: 2000-03-09</p> <p>; PRIOR APPLICATION NUMBER: DE 19930476.9</p> <p>; PRIOR FILING DATE: 1999-07-01</p> <p>; PRIOR APPLICATION NUMBER: DE 19931415.2</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931418.7</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931419.5</p>	<p>Query Match            38.0%;   Score 38;   DB 7;   Length 209;</p> <p>Best Local Similarity   44.4%;   Pred. No. 26;</p> <p>Matches     8;   Conservative     4;   Mismatches     6;   Indels     0;   Gaps     0;</p>	<p>QY        2   SGOAGAAASBSLFI SNHA 19</p> <p>Db        41   SGPAGLAQAQLTRAGHS 58</p>
<p>US-11-055-822-90</p> <p>; Sequence 90, Application US/11055822</p> <p>; Publication No. US20050260707A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Pompejus, Markus</p> <p>; APPLICANT: Kroger, Burkhard</p> <p>; APPLICANT: Schroder, Hartwig</p> <p>; APPLICANT: Zelder, Oskar</p> <p>; APPLICANT: Haberer, Gregor</p> <p>; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING</p> <p>; FILE REFERENCE: BGI-121CPCN</p> <p>; CURRENT APPLICATION NUMBER: US/11/055,822</p> <p>; CURRENT FILING DATE: 2005-02-11</p> <p>; PRIOR APPLICATION NUMBER: 09/606,740</p> <p>; PRIOR FILING DATE: 2000-06-23</p> <p>; PRIOR APPLICATION NUMBER: 60/141,031</p> <p>; PRIOR FILING DATE: 1999-06-25</p> <p>; PRIOR APPLICATION NUMBER: 60/142,101</p> <p>; PRIOR FILING DATE: 1999-07-02</p> <p>; PRIOR APPLICATION NUMBER: 60/148,613</p> <p>; PRIOR FILING DATE: 1999-08-12</p> <p>; PRIOR APPLICATION NUMBER: 60/187,970</p> <p>; PRIOR FILING DATE: 2000-03-09</p> <p>; PRIOR APPLICATION NUMBER: DE 19930476.9</p> <p>; PRIOR FILING DATE: 1999-07-01</p> <p>; PRIOR APPLICATION NUMBER: DE 19931415.2</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931418.7</p> <p>; PRIOR FILING DATE: 1999-07-08</p> <p>; PRIOR APPLICATION NUMBER: DE 19931419.5</p>	<p>Query Match            38.0%;   Score 38;   DB 7;   Length 209;</p> <p>Best Local Similarity   44.4%;   Pred. No. 26;</p> <p>Matches     8;   Conservative     4;   Mismatches     6;   Indels     0;   Gaps     0;</p>	<p>QY        2   SGOAGAAASBSLFI SNHA 19</p> <p>Db        41   SGPAGLAQAQLTRAGHS 58</p>
<p>US-11-055-822-90</p> <p>; Sequence 90, Application US/11055822</p> <p>; Publication No. US20050260707A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Pompejus, Markus</p> <p>; APPLICANT: Kroger, Burkhard</p> <p>; APPLICANT: Schroder, Hartwig</p> <p>; APPLICANT: Zelder, Oskar</p> <p>; APPLICANT: Haberer, Gregor</p> <p>; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM</p>		

; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 284  
; LENGTH: 1386  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Obtained from an environmental sample.  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)....(28)  
US-10-517-939-284

Query Match 38.0%; Score 38; DB 6; Length 1386;  
Best Local Similarity 44.4%; Pred. No. 2.2e+02;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SQAGAAASESLFISNHA 19  
Db 211 SGFEGRAGTETLTVTNEA 228

RESULT 15  
US-11-024-959-455  
; Sequence 455, Application US/11024959  
; Publication No. US20060010516A1  
; GENERAL INFORMATION:  
; APPLICANT: FORSTER, RICHARD L.  
; APPLICANT: CONNETT, MARIE B.  
; APPLICANT: EMERSON, SARAH JANE  
; APPLICANT: GRIGOR, MURRAY ROBERT  
; APPLICANT: HIGGINS, COLLEEN M.  
; APPLICANT: LUND, STEVEN TROY  
; APPLICANT: MAGUSIN, ANDREAS  
; APPLICANT: KODRZYCKI, BOB  
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS  
; FILE REFERENCE: 044463-0360  
; CURRENT APPLICATION NUMBER: US/11/024,959  
; CURRENT FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: 60/533,036  
; PRIOR FILING DATE: 2003-12-30  
; NUMBER OF SEQ ID NOS: 782  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 455  
; LENGTH: 327  
; TYPE: PRT  
; ORGANISM: Pinus radiata  
US-11-024-959-455

Query Match 37.0%; Score 37; DB 7; Length 327;  
Best Local Similarity 69.2%; Pred. No. 63;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 QGAGAAASESLFI 15  
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Search completed: February 10, 2006, 10:45:20  
Job time : 2.03321 secs

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2	28	100.0	28	6	AR010103	AR010103 Sequence
3	28	100.0	28	6	AR055309	AR055309 Sequence
4	28	100.0	28	6	AR141238	AR141238 Sequence
5	28	100.0	28	6	AR141475	AR141475 Sequence
6	28	100.0	28	6	II1949	II1949 Sequence 61
7	28	100.0	28	6	I40520	I40520 Sequence 59
8	28	100.0	28	6	AR368004	AR368004 Sequence
9	28	100.0	28	6	AR430985	AR430985 Sequence
10	24.8	88.6	813	6	AR003721	AR003721 Sequence
11	24.8	88.6	813	6	AR010057	AR010057 Sequence
12	24.8	88.6	813	6	AR055263	AR055263 Sequence
13	24.8	88.6	813	6	AR067747	AR067747 Sequence
14	24.8	88.6	813	6	AR141132	AR141132 Sequence
15	24.8	88.6	813	6	AR141429	AR141429 Sequence
16	24.8	88.6	813	6	AR164985	AR164985 Sequence
17	24.8	88.6	813	6	II1901	II1901 Sequence 11
18	24.8	88.6	813	6	II1947	II1947 Sequence 57

TITLE Immunotoxins comprising ribosome-inactivating proteins  
JOURNAL Patent: US 5756699-A 59 26-MAY-1998;  
FEATURES Location/Qualifiers  
source

ORIGIN /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CACATGTAACAAGACTTCATTTGGC 28

RESULT 3  
LOCUS AR055309 28 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 59 from patent US 5837491.  
ACCESSION AR055309  
VERSION AR055309.1 GI:5980886  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.  
TITLE Polynucleotides encoding gelonin sequences  
JOURNAL Patent: US 5837491-A 59 17-NOV-1998;  
FEATURES Location/Qualifiers  
source

ORIGIN /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTTGGC 28  
|||||  
Db 1 CACATGTAACAAGACTTCATTTGGC 28

RESULT 4  
LOCUS AR141238 28 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 59 from patent US 6146631.  
ACCESSION AR141238  
VERSION AR141238.1 GI:15100755  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.  
TITLE Immunotoxins comprising ribosome-inactivating proteins  
JOURNAL Patent: US 6146631-A 59 14-NOV-2000;  
FEATURES Location/Qualifiers  
source

ORIGIN /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTTGGC 28  
|||||  
Db 1 CACATGTAACAAGACTTCATTTGGC 28

RESULT 5  
LOCUS AR141475 28 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 59 from patent US 6146850.  
ACCESSION AR141475  
VERSION AR141475.1 GI:15100991  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Better,M.D. and Carroll,S.F.  
TITLE Proteins encoding gelonin sequences  
JOURNAL Patent: US 6146850-A 59 14-NOV-2000;  
FEATURES Location/Qualifiers  
source

ORIGIN /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTTGGC 28  
|||||  
Db 1 CACATGTAACAAGACTTCATTTGGC 28

RESULT 6  
LOCUS I11949 28 bp DNA linear PAT 26-JUL-1995  
DEFINITION Sequence 61 from Patent US 5416202.  
ACCESSION I11949  
VERSION I11949.1 GI:909392  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Lei,S.-P.  
TITLE Materials comprising and methods of preparation and use for  
ribosome-inactivating proteins  
JOURNAL Patent: US 5416202-A 61 16-MAY-1995;  
FEATURES Location/Qualifiers  
source

ORIGIN /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTTGGC 28  
|||||  
Db 1 CACATGTAACAAGACTTCATTTGGC 28

RESULT 7  
LOCUS I40520 28 bp DNA linear PAT 13-MAY-1997  
DEFINITION Sequence 59 from patent US 5621083.  
ACCESSION I40520  
VERSION I40520.1 GI:2082812  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.

TITLE Immunotoxins comprising ribosome-inactivating proteins  
JOURNAL Patent: US 5621083-A 59 15-APR-1997;  
FEATURES Location/Qualifiers  
source 1..28  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
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Db 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
|||||

RESULT 8  
AR368004  
LOCUS 28 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 59 from patent US 6376217.  
ACCESSION AR368004  
VERSION AR368004.1 GI:34601515  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Better,M.D. and Carroll,S.F.  
TITLE Fusion proteins and polynucleotides encoding gelonin sequences  
JOURNAL Patent: US 6376217-A 59 23-APR-2002;  
Xoma Technology Ltd.;;  
BMX;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
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RESULT 9  
AR430985  
LOCUS 28 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 59 from patent US 6649742.  
ACCESSION AR430985  
VERSION AR430985.1 GI:40192816  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.  
TITLE Immunotoxins comprising ribosome-inactivating proteins  
JOURNAL Patent: US 6649742-A 59 18-NOV-2003;  
XOMA Technology Ltd.;;  
BEX;  
FEATURES Location/Qualifiers  
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ORIGIN

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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
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RESULT 10  
AR003721  
LOCUS 813 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 11 from patent US 5744580.  
ACCESSION AR003721  
VERSION AR003721.1 GI:3964980  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.  
TITLE Immunotoxins comprising ribosome-inactivating proteins  
JOURNAL Patent: US 5744580-A 11 28-APR-1998;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 88.6%; Score 24.8; DB 6; Length 813;  
Best Local Similarity 92.9%; Pred. No. 14;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
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Db 303 CACAATTAAACAAGACTTCATTTTGGC 330  
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RESULT 11  
AR010057  
LOCUS 813 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 11 from patent US 5756699.  
ACCESSION AR010057  
VERSION AR010057.1 GI:3968862  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.  
TITLE Immunotoxins comprising ribosome-inactivating proteins  
JOURNAL Patent: US 5756699-A 11 26-MAY-1998;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 88.6%; Score 24.8; DB 6; Length 813;  
Best Local Similarity 92.9%; Pred. No. 14;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
|||||  
Db 303 CACAATTAAACAAGACTTCATTTTGGC 330  
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RESULT 12  
AR055263  
LOCUS 813 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 11 from patent US 5837491.  
ACCESSION AR055263  
VERSION AR055263.1 GI:5980840  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.  
TITLE Polynucleotides encoding gelonin sequences  
JOURNAL Patent: US 5837491-A 11 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..813  
/organism="unknown"  
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ORIGIN  
Query Match 88.6%; Score 24.8; DB 6; Length 813;  
Best Local Similarity 92.9%; Pred. No. 14;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
DB 303 CACAATTAATAACAAGACTTCATTTTGGC 330  
RESULT 13  
LOCUS AR067747 813 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 246 from patent US 5851802.  
ACCESSION AR067747  
VERSION AR067747.1 GI:5998969  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Better,M.D.  
TITLE Methods for recombinant microbial production of fusion proteins and BPI-derived peptides  
JOURNAL Patent: US 5851802-A 246 22-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..813  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 88.6%; Score 24.8; DB 6; Length 813;  
Best Local Similarity 92.9%; Pred. No. 14;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
DB 303 CACAATTAATAACAAGACTTCATTTTGGC 330  
RESULT 14  
LOCUS AR141192 813 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 11 from patent US 6146631.  
ACCESSION AR141192  
VERSION AR141192.1 GI:15100709  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.  
TITLE Immunotoxins comprising ribosome-inactivating proteins  
JOURNAL Patent: US 6146631-A 11 14-NOV-2000;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
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Best Local Similarity 92.9%; Pred. No. 14;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
DB 303 CACAATTAATAACAAGACTTCATTTTGGC 330  
RESULT 15  
LOCUS AR141429 813 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 11 from patent US 6146850.  
ACCESSION AR141429  
VERSION AR141429.1 GI:15100945  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Better,M.D. and Carroll,S.F.  
TITLE Proteins encoding gelonin sequences  
JOURNAL Patent: US 6146850-A 11 14-NOV-2000;  
FEATURES Location/Qualifiers  
source 1..813  
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/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 88.6%; Score 24.8; DB 6; Length 813;  
Best Local Similarity 92.9%; Pred. No. 14;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACATGTAATAACAAGACTTCATTTTGGC 28  
DB 303 CACAATTAATAACAAGACTTCATTTTGGC 330  
Search completed: February 13, 2006, 14:37:41  
Job time : 1743 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2006, 23:16:37 ; Search time 271 Seconds  
(without alignments)  
688.603 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAAACAGACTTCATTTGGC 28

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	2	AAQ42253 PCR prime
2	24.8	88.6	813	2	AAQ48031 Encodes p
3	24.8	88.6	813	2	AAQ42222 Encodes p
4	24.8	88.6	813	2	AAQ75532 Type I ri
5	24.8	88.6	813	2	AAQ92342 Type I ri
6	24.8	88.6	955	2	AAQ86336 BPI pepti
7	24.8	88.6	1003	2	AAQ86341 BPI pepti
8	24.8	88.6	1072	2	AAQ86332 BPI pepti
9	24.8	88.6	1176	6	AB56021 cDNA enco
10	24.8	88.6	1500	14	AB568721 scFv23-ge
11	24.8	88.6	1527	6	AB56029 DNA encod
12	20.6	73.6	38142	13	ABD32682 Mouse can
13	20.2	72.1	2103	8	ACF73271 Staphyloc
14	20.2	72.1	2187	2	AAV74640 Staphyloc
15	20	71.4	11298	2	AAV86756 Human hlg
16	20	71.4	11298	2	AAV54661 Human bet
17	20	71.4	11298	3	AAQ4815 Human ade
18	20	71.4	11298	3	AAQ20937 Human hlg
19	20	71.4	11298	4	AAQ92144 Human IGE

20	20	71.4	11298	10	ABZ96631 Human hlg
21	20	71.4	11298	11	ABD19056 Human hlg
22	20	71.4	11357	2	AAQ51024 Human FCB
23	20	71.4	21742	3	AAQ34816 Human ade
24	20	71.4	21742	3	AAQ20938 Human hlg
25	20	71.4	21742	10	ABZ96632 Human hlg
26	20	71.4	21742	11	ABD19051 Human hlg
27	20	71.4	33030	5	AAQ29337 Atopy rel
28	20	71.4	117608	10	ABZ97129 Human rec
29	20	71.4	117609	3	AAQ21435 Human rec
30	20	71.4	117609	11	ABD17968 Human rec
31	19.8	70.7	1637	6	AAQ43749 Human AGT
32	19.8	70.7	2361	6	AAQ43751 Human AGT
33	19.8	70.7	2361	6	AAQ43821 Human AGT
34	19.8	70.7	4102	6	AAQ18667 Reference
35	19.8	70.7	4788	2	AAQ85367 MIP-1-1p
36	19.6	70.0	2949	8	ACF03675 Human eph
37	19.6	70.0	2953	6	ABV78119 Human eph
38	19.6	70.0	2953	6	ABZ35695 Human eph
39	19.6	70.0	2953	6	ABX09338 Human eph
40	19.6	70.0	2953	6	ABL91660 Human pol
41	19.6	70.0	3132	2	AAQ34513 HEK codin
42	19.6	70.0	3149	3	AAQ64458 CDNA enco
43	19.6	70.0	3149	8	ABZ34862 Coding se
44	19.6	70.0	3149	10	AAQ58484 Human rec
45	19.6	70.0	3149	10	ABZ75272 Prostate

## ALIGNMENTS

### RESULT 1

AAQ42253  
ID AAQ42253 standard; cDNA; 28 BP.

AC AAQ42253;

DT 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

DE PCR primer Geloc-20 to replace Ile103 of gelonin with Cys.

KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;

KW autoimmune disease; cell killing; toxin;

KW Mutagenic polymerase chain reaction; ss.

OS Synthetic.

XX WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US009487.

XX 04-NOV-1991; 91US-00787567.

XX 19-JUN-1992; 92US-00901707.

XX (XOMA ) XOMA CORP.

XX Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI, 1993-167617/20.

XX Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating autoimmune diseases, cancer, graft versus host disease and selective cell killing in vivo.

XX Example 3; Page 35; 163pp; English.

XX Fifteen analogues of gelonin were constructed. Ten non-cysteine residues in surface positions and available for conjugation to a second protein were targeted for substn. In the other analogues, one or both of the native Cys residues present in gelonin were substd. Overlap extension PCR

CC was used to construct the various analogues. Primer geloC-20 was used in  
 CC the subseq. of Ile103 of gelonin by Cys. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

SQ Sequence 28 BP; 10 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.051; 0; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAAACAAGACTTCATTGGC 28  
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 Db 1 CACATGTAAACAAGACTTCATTGGC 28

## RESULT 2

AAQ48031  
 ID AAQ48031 standard; cDNA; 813 BP.

XX AC AAQ48031;

XX DT 25-MAR-2003 (revised)  
 DT 13-SEP-1993 (first entry)

XX DE Encodes plant type I RIP Gelonin.

XX KW Type I ribosome-inactivating protein; ricin; immunoconjugate;  
 KW autoimmune disease; cell killing; toxin; Euphorbiaceae family.

XX OS Gelonium multiflorum.

XX PN W09309130-A1.

XX PD 13-MAY-1993.

XX PF 04-NOV-1992; 92WO-US009487.

XX PR 04-NOV-1991; 91US-00787567.

XX PR 19-JUN-1992; 92US-00901707.

XX PA (XOMA) XOMA CORP.

XX PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX DR WPI; 1993-167617/20.

XX PT Analogues of type I ribosome inactivating protein - useful as cytotoxic  
 PT agents, immuno toxins for treating autoimmune diseases, cancer, graft  
 PT versus host disease and selective cell killing in-vivo.

XX PS Claim 85; Page 114; 163pp; English.

XX CC The invention covers analogues of Type I RIPs. Gelonin is a Type I RIP  
 CC and the analogues of the invention have a cysteine available for  
 CC intermolecular disulphide bonding at an amino acid position corresp. to a  
 CC position not naturally available for bonding; the cysteine residue is located  
 CC in the C-terminal region of the analogue between a position corresp. to  
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are  
 CC pref. joined via a disulphide linkage to a molecule which specifically  
 CC binds to a target cell, e.g. an antibody fragment. See AAR37291 for  
 CC gelonin amino acid sequence. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

SQ Sequence 813 BP; 266 A; 150 C; 182 G; 215 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;  
 Best Local Similarity 92.9%; Pred. No. 1.6; 0; Indels 0; Gaps 0;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAAACAAGACTTCATTGGC 28  
 |||||  
 Db 303 CACATGTAAACAAGACTTCATTGGC 330

## RESULT 3

AAQ42222  
 ID AAQ42222 standard; cDNA; 813 BP.

XX AC AAQ42222;

XX DT 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

XX DE Encodes plant type I RIP Gelonin.

XX KW Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;  
 KW autoimmune disease; cell killing; toxin; Euphorbiaceae family; ss.

XX OS Gelonium multiflorum.

XX PN W09309130-A1.

XX PD 13-MAY-1993.

XX PF 04-NOV-1992; 92WO-US009487.

XX PR 04-NOV-1991; 91US-00787567.

XX PR 19-JUN-1992; 92US-00901707.

XX PA (XOMA) XOMA CORP.

XX PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX DR WPI; 1993-167617/20.

XX PT Analogues of type I ribosome inactivating protein - useful as cytotoxic  
 PT agents, immuno toxins for treating autoimmune diseases, cancer, graft  
 PT versus host disease and selective cell killing in-vivo.

XX PS Claim 85; Page 101; 163pp; English.

XX CC Proteolytic peptide fragments of native gelonin were sequenced. PCR  
 CC primers were designed based on these peptide fragments. The primers were  
 CC used to amplify segments of cDNA covering the 5'-terminal, middle and 3'-  
 CC terminal regions of the gelonin coding sequence. A composite gelonin gene  
 CC sequence was assembled from the overlapping gelonin DNA fragments (see  
 CC AAQ42222). Having cloned the gelonin gene, the development of gelonin  
 CC analogues and gene fusions is facilitated. See AAR37291 for gelonin amino  
 CC acid sequence. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;

Best Local Similarity 92.9%; Pred. No. 1.6;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAAACAAGACTTCATTGGC 28

|||||

Db 303 CACATGTAAACAAGACTTCATTGGC 330

## RESULT 4

AAQ75532

ID AAQ75532 standard; cDNA; 813 BP.

XX AC AAQ75532;

XX DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX DE Type I ribosome-inactivating protein gelonin cDNA.

XX KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease; ss.

```

OS Gelonium multiflorum.
XX
XX Key Location/Qualifiers
XX mat_peptide 1..810
XX /*tag= a
XX /transl_except= pos:754..810
XX /note= "no corresponding amino acids"
XX
XX WO9426910-A1.
XX
XX PD 24-NOV-1994.
XX
XX PF 12-MAY-1994; 94WO-US005348.
XX
XX PR 12-MAY-1993; 93US-00064691.
XX
XX PA (XOMA ) XOMA CORP.
XX
XX PI Better MD, Carroll SF, Studnicka GM;
XX WPI; 1995-006804/01.
XX DR P-PSDB; AAR63903.
XX
XX PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
XX are suitable for use as components of cytotoxic therapeutic agents.
XX
XX PS Example 1; Page 155; 22ipp; English.
XX
XX CC AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)
XX gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key
XX components of cytotoxic therapeutic agents (CTAs), which include gene
XX fusion products and immunoconjugates. CTAs may be used to selectively
XX eliminate any cell type to which a RIP component is targeted, by the
XX specific binding capacity of the second component of the agent. They can
XX be used in the treatment of diseases where the elimination of a
XX particular cell type is desired, such as autoimmune disease, cancer and
XX graft-versus-host disease. (Updated on 25-MAR-2003 to correct FN field.)
XX
XX SQ Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CACATGTAAACACAGACTTCATTTGGC 28
Db 303 CACAATTAACACAGACTTCATTTGGC 330

RESULT 5
ID AAQ92342 standard; DNA; 813 BP.
AC AAQ92342;
XX
XX DT 25-MAR-2003 (revised)
XX DT 01-JAN-1996 (first entry)
XX
XX DE Type I ribosome-inactivating protein gelonin gene.
XX
XX KW Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin; ss.
XX OS Gelonium multiflorum.
XX
XX PN US5416202-A.
XX
XX PD 16-MAY-1995.
XX
XX PF 09-DEC-1992; 92US-00988430.
XX
XX PR 04-NOV-1991; 91US-00787567.
XX PR 19-JUN-1992; 92US-00901707.
XX

PA (XOMA ) XOMA CORP.
XX
XX PI Lei S, Carroll SF, Lane JA, Bernhard SL, Better MD;
XX WPI; 1995-193480/25.
XX
XX PT Polynucleotide(s) encoding gelonin analogues - having a cysteine residue
XX for intermolecular bonding for the prodn. of immuno-toxin(s).
XX
XX PS Example; Col 71-72; 66pp; English.
XX
XX CC Analogues of Type I RIP are defined as non-naturally occurring
XX polypeptides that share the ribosome-inactivating activity of the natural
XX protein but differ in AA sequence. Preferred analogues have a Cys
XX available for disulfide bonding located at a posn. it its AA sequence
XX from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy
XX terminus of the analogue. (AAR74176 is the sequence of ricin A-chain RTA,
XX which is a Type II RIP). The primary AA sequence of the Type I RIPs
XX gelonin, BRIP, mormordin II, luffin [see Islam et al. Agricultural
XX Biological Chem., 54(5) 1343-45 1991], alphatrachosanthin [see Chow et
XX al., J. Biol. Chem., 265, 8670-74 1990], momordin I [see Ho et al., BBA,
XX 1088, 311-14 1991], Mirabilis antiviral protein [see Habuka et al., J.
XX Biol. Chem., 264(12) 6629-37 1989], pokeweed antiviral protein isolated
XX from seeds [see Kung et al., Agric. Biol. Chem., 54(12), 3301-18 1990]
XX and saporin [see Banatti et al., Eur. J. Biochem., 183, 465-70 1989] are
XX individually aligned with the primary sequence of the ricin A-chain [see
XX Halling et al., Nucleic Acids Res., 13, 8019-8033 1985] respectively in
XX Figures 1-9. The AAs invariant among the ricin A-chain and the Type I
XX RIPs are indicated in FT. Also indicated are the preferred sites of Cys
XX substitution. It is also preferred that the gelonin cysteine residues at
XX positions 44 and 50 be replaced with alanine residues. The complete DNA
XX sequence of the gelonin gene is set out in AAQ92342. (Updated on 25-MAR-
XX 2003 to correct PR field.)
XX
XX SQ Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CACATGTAAACACAGACTTCATTTGGC 28
Db 303 CACAATTAACACAGACTTCATTTGGC 330

RESULT 6
ID AAT86336 standard; DNA; 955 BP.
XX
XX AC AAT86336;
XX
XX DT 20-APR-1998 (first entry)
XX
XX DE BPI peptide fusion protein pING3797 vector construct.
XX
XX KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
XX KW fungicidal; recombinant DNA; vector; ss.
XX
XX OS Synthetic.
XX OS Pectobacterium carotovorum.
XX OS Homo sapiens.
XX OS Chimeric.
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XX /standard_name= "Leader"
XX /note= "pel B is the leader sequence from the pectate
XX lyase gene of Erwinia carotovora"
XX 23..273
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XX /*tag= b

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FT /label= gelonin
FT /note= "gelonin - see U.S. Patent No. 5,416,202"
FT CDS 66..944
FT /*tag= c
FT misc_feature 274..275
FT /*tag= d
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FT /note= "BPI-derived peptide"
XX
XX WO9735009-A1.
XX
XX 25-SEP-1997.
XX
XX 18-MAR-1997; 97WO-US005287.
XX
XX 22-MAR-1996; 96US-00621803.
XX (XOMA ) XOMA CORP.
XX
XX Better MD;
XX
XX WPI; 1997-480215/44.
XX P-PSDB; AAW29300.
XX
XX Recombinant production of bactericidal/permeability increasing protein -
XX by expression as a fusion protein in microbial host cells, then cleaving
XX the BPI peptide from the carrier.
XX
XX Example 1; Page 160-161; 186pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes a
XX fusion protein and is suitable for introduction into a bacterial host.
XX The vector comprises: (a) DNA encoding at least one cationic
XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX located between (a) and (b). The present sequence represents the pING3797
XX vector construct coding for a BPI fusion protein. The peptides have many
XX uses including the treatment of bacterial and fungal infections. BPI
XX peptides also bind to endotoxins and heparin, neutralising their effects.
XX The peptides have further been shown to inhibit angiogenesis (partly due
XX to heparin-binding activity). The fusion proteins have been found to be
XX expressed in large amounts without significant proteolysis, and in some
XX cases are actually secreted from the host cells. This allows the indirect
XX production of anti-microbial BPI peptides in microbial hosts
XX
XX Sequence 955 BP; 307 A; 189 C; 216 G; 243 T; 0 U; 0 Other;
XX
XX Query Match 88.6%; Score 24.8; DB 2; Length 955;
XX Best Local Similarity 92.9%; Pred. No. 1.6;
XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CACATGTAACCAAGACTTCATTGGC 28
XX ||||| ||||| ||||| ||||| |||||
XX Db 434 CACAATTAACCAAGACTTCATTGGC 461
XX
XX RESULT 7
XX AAT86341
XX ID AAT86341 standard; DNA; 1003 BP.
XX
XX AAT86341;
XX
XX 20-APR-1998 (first entry)
XX
XX

```

```

DE BPI peptide fusion protein pING3795 vector construct.
XX
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
XX fungicidal; recombinant DNA; vector; ss.
XX
XX Synthetic.
XX Pectobacterium carotovorum.
XX Homo sapiens.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX misc_signal 1..22
XX /*tag= a
XX /label= pel_B
XX /standard_name= "Leader"
XX /note= "pel B is the leader sequence from the pectate
XX lyase gene of Erwinia caratovora"
XX 23..273
XX /*tag= b
XX /label= gelonin
XX /note= "gelonin - see U.S. Patent No. 5,416,202"
XX 66..992
XX /*tag= c
XX 274..275
XX /*tag= d
XX /label= EagI
XX /note= "EagI cloning site"
XX 276..279
XX /*tag= g
XX /label= cleavage linker
XX /note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
XX cleavage site"
XX 280..309
XX /*tag= h
XX /label= peptide sequence
XX /note= "BPI-derived peptide"
XX
XX WO9735009-A1.
XX
XX 25-SEP-1997.
XX
XX 18-MAR-1997; 97WO-US005287.
XX
XX 22-MAR-1996; 96US-00621803.
XX (XOMA ) XOMA CORP.
XX
XX Better MD;
XX
XX WPI; 1997-480215/44.
XX P-PSDB; AAW29303.
XX
XX Recombinant production of bactericidal/permeability increasing protein -
XX by expression as a fusion protein in microbial host cells, then cleaving
XX the BPI peptide from the carrier.
XX
XX Example 1; Page 152-153; 186pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes a
XX fusion protein and is suitable for introduction into a bacterial host.
XX The vector comprises: (a) DNA encoding at least one cationic
XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX located between (a) and (b). The present sequence represents the pING3795
XX vector construct coding for a BPI fusion protein. The peptides have many
XX uses including the treatment of bacterial and fungal infections. BPI
XX peptides also bind to endotoxins and heparin, neutralising their effects.
XX The peptides have further been shown to inhibit angiogenesis (partly due
XX to heparin-binding activity). The fusion proteins have been found to be
XX expressed in large amounts without significant proteolysis, and in some
XX cases are actually secreted from the host cells. This allows the indirect
XX production of anti-microbial BPI peptides in microbial hosts
XX
XX Sequence 955 BP; 307 A; 189 C; 216 G; 243 T; 0 U; 0 Other;
XX
XX Query Match 88.6%; Score 24.8; DB 2; Length 955;
XX Best Local Similarity 92.9%; Pred. No. 1.6;
XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CACATGTAACCAAGACTTCATTGGC 28
XX ||||| ||||| ||||| ||||| |||||
XX Db 434 CACAATTAACCAAGACTTCATTGGC 461
XX
XX RESULT 7
XX AAT86341
XX ID AAT86341 standard; DNA; 1003 BP.
XX
XX AAT86341;
XX
XX 20-APR-1998 (first entry)
XX
XX

```



XX	(XOMA ) XOMA CORP.
XX	Better MD;
XX	WPI; 1997-480215/44.
DR	P-PSDB; AAW29294.
XX	
PT	Recombinant production of bactericidal/permeability increasing protein -
PT	by expression as a fusion protein in microbial host cells, then cleaving
PT	the BPI peptide from the carrier.
XX	
PS	Example 1; Page 148-150; 186pp; English.
XX	
CC	A new recombinant DNA vector construct has been developed which encodes a
CC	fusion protein and is suitable for introduction into a bacterial host.
CC	The vector comprises: (a) DNA encoding at least one cationic
CC	bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC	carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC	located between (a) and (b). The present sequence represents the pING3793
CC	vector construct coding for a BPI fusion protein. The peptides have many
CC	uses including the treatment of bacterial and fungal infections. BPI
CC	peptides also bind to endotoxins and heparin, neutralising their effects.
CC	The peptides have further been shown to inhibit angiogenesis (partly due
CC	to heparin-binding activity). The fusion proteins have been found to be
CC	expressed in large amounts without significant proteolysis, and in some
CC	cases are actually secreted from the host cells. This allows the indirect
CC	production of anti-microbial BPI peptides in microbial hosts
XX	
XX	Sequence 1072 BP; 340 A; 210 C; 244 G; 278 T; 0 U; 0 Other;
SQ	
	Query Match 88.6%; Score 24.8; DB 2; Length 1072;
	Best Local Similarity 92.9%; Pred. No. 1.6;
	Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 CACATGTAATAACAAGACTTCATTGTC 28
DB	434 CACATTAATAACAAGACTTCATTGTC 461
RESULT 9	
ABSS56021	
ID	ABSS56021 standard; cDNA; 1176 BP.
XX	
AC	ABSS56021;
XX	
DT	08-JAN-2003 (first entry)
XX	
DE	cDNA encoding G. multiflorum recombinant gelonin (rGel) toxin.
XX	
KW	Modified protein; reduced antigenicity; modified toxin; gelonin;
KW	designer toxin; immunotoxin; proteinaceous compound; cancer;
KW	microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW	autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW	inflammatory disease; cardiovascular disease; diabetes;
KW	pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW	cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW	recombinant gelonin; rGel; gene; ss.
XX	
OS	Gelonium multiflorum.
XX	
Key	Location/Qualifiers
FT	24..974
CDS	/*tag= a
FT	/product= "rGel"
FT	
XX	
XX	WO200269886-A2.
XX	
PN	
PD	12-SEP-2002.
XX	
PF	12-FEB-2002; 2002WO-US0004195.
XX	
PR	12-FEB-2001; 2001US-0268402P.
XX	



```
PT /product= "scfWEL/rGel fusion protein"
XX WO200269886-A2.
XX 12-SEP-2002.
XX
XX 12-FEB-2002; 2002WO-US004195.
XX
XX 12-FEB-2001; 2001US-0268402P.
XX (RBR-) RES DEV FOUND.
XX
XX Rosenblum MG, Cheung L;
XX
XX WPI; 2002-750431/81.
XX P-PSDB; ABG71552.
XX
XX Generating a modified protein with reduced antigenicity for treating
XX cancer, AIDS, autoimmune diseases, comprises identifying a protein region
XX antigenic in the first subject using antiserum from either the first or a
XX second subject.
XX
XX Example 5; Fig 5; 176pp; English.
XX
XX The present invention relates to a method of generating a modified
XX protein with reduced antigenicity while maintaining its biological
XX activity. The method comprises identifying a region of the protein that
XX is antigenic in a first subject using antiserum from either the first
XX subject or a second subject of the same species as the first subject. In
XX particular the invention discloses modified toxin compounds, for example
XX gelonin toxin derived from Geonium multiflorum, that are truncated
XX and/or possess reduced antigenicity. Such designer toxins have
XX therapeutic, diagnostic, and preventative benefits, particularly as
XX immunotoxins. The method of the invention is useful for generating
XX proteinaceous compounds with less antigenicity. The immunotoxin and
XX gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
XX skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
XX bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
XX bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
XX compositions of the invention are also useful for treating microbial
XX pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
XX diseases, hyperproliferative disorders including cancer, leukaemias,
XX arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
XX diseases, and diabetes. The method provides less antigenic proteins,
XX peptides and polypeptides, which are more effective than prior art. The
XX present sequence encodes murine single-chain ZME-018 antibody/G.
XX multiflorum recombinant gelonin (rGel) (scfWEL/rGel) fusion protein
XX
XX Sequence 1527 BP; 458 A; 320 C; 367 G; 382 T; 0 U; 0 Other;
XX
XX Query Match 88.6%; Score 24.8; DB 6; Length 1527;
XX Best Local Similarity 92.9%; Pred. No. 1.7;
XX Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 CACATGTAAACACAGACTTCATTTGGC 28
XX |||||
XX Db 1071 CACATTAACACAGACTTCATTTGGC 1098
XX
XX RESULT 12
XX ABD32682
XX ID ABD32682 standard; DNA; 38142 BP.
XX
XX AC ABD32682;
XX
XX 18-NOV-2004 (first entry)
XX
XX Mouse cancer-associated genomic DNA MD13-117.
XX
XX Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
XX leukaemia; lymphoma; CAP.
XX
XX Mus musculus.
```

```
XX WO2004074320-A2.
XX
XX 02-SEP-2004.
XX
XX 17-FEB-2004; 2004WO-US004730.
XX
XX 14-FEB-2003; 2003US-00367094.
XX 14-MAR-2003; 2003US-00388838.
XX 15-APR-2003; 2003US-00417375.
XX 13-JUN-2003; 2003US-00461862.
XX 15-SEP-2003; 2003US-00663431.
XX 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
XX
XX WPI; 2004-652914/63.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.
XX
XX disclosure; seqid 236; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
XX in the specification, or its complement. The nucleic acids encode cancer-
XX associated proteins. Also included are an expression vector comprising
XX the isolated nucleic acid cited above, a host cell comprising the above
XX recombinant nucleic acid or expression vector, a microarray for detecting
XX a cancer-associated (CA) nucleic acid comprising at least one probe
XX comprising at least 10 contiguous nucleotides of any of the above-
XX mentioned nucleotide sequences, an isolated polypeptide (encoded within
XX an open reading frame of a CA sequence selected from any of the 95
XX polynucleotide sequences as mentioned in the specification, or its
XX complement), an isolated antibody, (or its antigen binding fragment) that
XX binds to the above polypeptide, a hybridoma that produces the above
XX monoclonal antibody, a pharmaceutical composition comprising the above
XX antibody and a pharmaceutical excipient, a kit for detecting cancer
XX cells (comprising the antibody cited above, methods for diagnosing cancer
XX or for detecting the presence or absence of cancer cells in an
XX individual, a method for inhibiting growth of cancer cells in an
XX individual, a method for delivering a therapeutic agent to cancer cells
XX in an individual, an electronic library comprising the above
XX polynucleotide or polypeptide (or their fragments), methods of screening
XX for anticancer activity or for a bioactive agent capable of modulating
XX the activity of a CA protein (CAP), methods for detecting cancer
XX associated with expression of a polypeptide in a test cell sample, a
XX method for treating cancers and a method for inhibiting the expression of
XX CA gene in a cell. The composition and methods are useful for detecting,
XX diagnosing, preventing and treating cancers, especially lymphoma and
XX leukaemia. These may also be used in screening for agents that modulate
XX cancer. The present sequence is a mouse CAP genomic sequence. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 38142 BP; 10396 A; 8310 C; 8130 G; 10863 T; 0 U; 443 Other;
XX
XX Query Match 73.6%; Score 20.6; DB 13; Length 38142;
XX Best Local Similarity 85.2%; Pred. No. 1.3e+02;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX Qy 1 CACATGTAAACACAGACTTCATTTGG 27
XX |||||
XX Db 16568 CAGATGGAACACAGACTTCAGTGTGG 16594
XX
XX RESULT 13
XX ACF73271
XX ID ACF73271 standard; DNA; 2103 BP.
```

```

XX ACF73271;
AC
XX 20-NOV-2003 (first entry)
DT
XX Staphylococcus aureus DNA #951.
DE
XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target; gene; ds.
KW
XX Staphylococcus aureus.
OS
XX WO200294868-A2.
PN
XX 28-NOV-2002.
PD
XX 27-MAR-2002; 2002WO-IB002637.
PF
XX 27-MAR-2001; 2001GB-00007661.
PR
XX (CHIR-) CHIRON SPA.
PA
XX Masignani V, Mora M, Scarselli M;
PI
XX WPI; 2003-120786/11.
DR
XX P-PSDB; ABW71711.
DR
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
XX Claim 6; SEQ ID NO 1901; 49pp; English.
PS
XX The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus genes of the invention
XX
XX Sequence 2103 BP; 786 A; 330 C; 271 G; 716 T; 0 U; 0 Other;
SQ
Query Match 72.1%; Score 20.2; DB 8; Length 2103;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CACATGTAACCAAGACTTCATTTT 25
Db 1838 CAGACGTAACCAAGACTTCATTTT 1862
RESULT 14
AAV74640
ID AAV74640 standard; DNA; 2187 BP.
XX
AC AAV74640;
XX
DT 16-MAR-1999 (first entry)
XX
XX Staphylococcus aureus contig SEQ ID #329.
DE
XX Computer readable medium; vaccine; S. aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
XX
OS Staphylococcus aureus.
XX
XX Key Location/Qualifiers
PH

```

```

FT misc_feature 1321..1380
FT /*tag= a
FT /note= "these bases represent a line of missing text in
FT the sequence listing in the specification. They are
FT included to maintain the nucleotide numbering given in
FT the specification for this DNA sequence"
XX
PN EP786519-A2.
XX
XX 30-JUL-1997.
PD
XX 07-JAN-1997; 97EP-00100117.
PF
XX 05-JAN-1996; 96US-0009861P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
PI
XX WPI; 1997-374922/35.
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S. aureus vaccines.
XX
XX Claim 1; Page 1197-1198; 3271pp; English.
PS
XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S. aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S. aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S. aureus in a sample. S. aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S. aureus DNA sequences contained on the computer
CC readable medium
XX
XX Sequence 2187 BP; 780 A; 328 C; 334 G; 683 T; 0 U; 62 Other;
SQ
Query Match 72.1%; Score 20.2; DB 2; Length 2187;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CACATGTAACCAAGACTTCATTTT 25
Db 451 CAGACGTAACCAAGACTTCATTTT 475
RESULT 15
AAT86756
ID AAT86756 standard; DNA; 11298 BP.
XX
AC AAT86756;
XX
XX 12-DEC-1997 (first entry)
DT
XX Human high affinity IgE receptor beta chain E237G variant gene.
DE
XX human; immunoglobulin E; high affinity receptor; beta subunit; IgE;
KW Fc epsilon RI beta; exon 7; variant; E237G; atopy; atopic asthma;
KW detection; diagnosis; polymorphism; subgroup; clinical management; ss.
XX
XX Homo sapiens.
OS
XX

```

FH Key Location/Qualifiers

FT exon 354. .511  
FT /tag= a  
FT /number= 1  
FT intron 512. .1380  
FT /tag= b  
FT /number= 1  
FT exon 1381. .1510  
FT /tag= c  
FT intron 1511. .2025  
FT /tag= d  
FT /number= 2  
FT exon 2026. .2160  
FT /tag= e  
FT intron 2161. .4474  
FT /tag= f  
FT /number= 3  
FT exon 4475. .4531  
FT /tag= g  
FT intron 4532. .5078  
FT /tag= h  
FT /number= 4  
FT exon 5079. .5237  
FT /tag= i  
FT intron 5238. .5639  
FT /tag= j  
FT /number= 5  
FT exon 5640. .5738  
FT /tag= k  
FT intron 5739. .7223  
FT /tag= l  
FT /number= 6  
FT exon 7224. .10214  
FT /tag= m  
FT /number= 7  
FT variation 7297  
FT /tag= n  
FT /note= "nucleotide change from wild type adenine to  
FT guanine"  
PN WO9708338-A1.  
XX PD 06-MAR-1997.  
XX PF 29-AUG-1996; 96WO-GB002095.  
XX PR 29-AUG-1995; 95GB-00017585.  
XX PA (ISIS-) ISIS INNOVATIONS LTD.  
XX PI Cookson WOC, Hill MR;  
XX WPI; 1997-179293/16.  
XX P-PSDB; AAW29149.  
XX Diagnosing atopy, or predisposition to it - by detection of  
FT immunoglobulin E high affinity receptor beta subunit exon 7 variant  
FT Glu237Gly.  
XX PS Disclosure; Page; 25pp; English.  
XX This DNA encodes human immunoglobulin E (IgE) high affinity receptor beta  
CC subunit (Fc epsilon RI beta ) exon 7 variant E237G. This variant is  
CC associated with atopy and atopic asthma. The variation is in exon 7 and  
CC is a nucleotide change from adenine to guanine at nucleotide 7297  
CC (nucleotide 6843 in the Fc epsilon RI beta gene sequence of Kuster, et  
CC al. 1992). Detection of the protein is useful for diagnosis of atopy. In  
CC particular the E273G polymorphism may also define a subgroup of asthma

CC suffers with a particular clinical course, in which case recognition of  
CC the variant/polymorphism would be of value in defining asthma prognosis  
CC and management. NB. This sequence was created using the sequence given in  
CC Genbank M89796  
XX  
SQ Sequence 11298 BP; 3469 A; 2113 C; 2284 G; 3415 T; 0 U; 17 Other;  
Query Match 71.4%; Score 20; DB 2; Length 11298;  
Best Local Similarity 82.1%; Pred. No. 2.1e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CACATGTAAACAAGACTTCATTGTC 28  
||||| ||||||| ||||||| |||||  
Db 4423 CACATTGAAACAAGACTTCATTGTC 4450  
Search completed: February 13, 2006, 00:02:17  
Job time : 273 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 14, 2006, 04:02:19 ; Search time 1924 Seconds  
(without alignments)  
680.893 Million cell updates/sec

Title: us-10-717-243-59  
Perfect score: 28  
Sequence: 1 CACATGTAACACAGACTTCATTTGGC 28

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hic:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.2	79.3	540	10 BX992195	Forward s
2	21.6	77.1	835	11 CNS03C2M	AL237271 Tetraodon
3	21.6	77.1	1013	9 CC279684	CC279684 CH261-76J
4	21.6	77.1	1128	9 CC214234	CC214234 CH261-74J
5	21.2	75.7	834	7 CO646793	CO646793 ILLUMIGEN
6	21.2	75.7	942	4 AY066661	AY066661 Schmidtea
7	20.8	74.3	464	2 BE581909	BE581909 kq56c05.y
8	20.8	74.3	642	10 BX199941	BX199941 Danilo rer
9	20.8	74.3	652	9 CE147952	CE147952 tigr-ges-
10	20.6	73.6	546	9 BH341834	BH341834 CH230-64E
11	20.6	73.6	576	7 CN951902	CN951902 Ha mx0 53
12	20.6	73.6	598	5 BX859292	BX859292 BX859292
13	20.6	73.6	659	11 CR033848	CR033848 Forward s
14	20.6	73.6	725	7 CN949957	CN949957 Ha mx0 27
15	20.6	73.6	759	9 BZ462328	BZ462328 BOOAA76TR
16	20.6	73.6	768	2 BG921708	BG921708 602825533
17	20.6	73.6	789	9 AQ049899	AQ049899 nbx50003a
18	20.6	73.6	802	10 CZ307473	CZ307473 ZMMPF0003
19	20.6	73.6	825	10 CW715575	CW715575 A1AA-aab9
20	20.2	72.1	443	1 AV987297	AV987297 AV987297
21	20.2	72.1	456	1 AV998061	AV998061 AV998061
22	20.2	72.1	495	8 DN897715	DN897715 nap24h08.

23	20.2	72.1	529	2 BG949978	BG949978 PM2-BN013
24	20.2	72.1	556	6 CD665396	CD665396 EtESTeg43
25	20.2	72.1	682	10 CW104570	CW104570 104 473 1
26	20.2	72.1	690	10 CW173871	CW173871 104 585 1
27	20.2	72.1	693	10 CW094316	CW094316 104 457 1
28	20.2	72.1	857	10 DU070222	DU070222 137839 To
29	20.2	72.1	875	10 CNS02890	AL211653 Tetraodon
30	20.2	72.1	880	10 CL677144	BZ229732 CH230-527
31	20.2	72.1	882	9 BZ229732	CZ317278 ZMMPF0017
32	20.2	72.1	919	10 CZ317278	BG627700 CC-esf1cL
33	20	71.4	361	2 BG627700	CO081295 GR Ra45E
34	20	71.4	396	7 CO081295	B1512246 BBI60008B
35	20	71.4	407	3 B1512246	B1511101 BBI60004B
36	20	71.4	466	3 B1511101	AI432231 th43c06.x
37	20	71.4	494	1 AI432231	BF567678 UI-R-B00-
38	20	71.4	555	2 BF567678	CO096633 GR Ra24K
39	20	71.4	555	7 CO096633	CO094330 GR_Ea16P
40	20	71.4	651	7 CO094330	BG127096 EST472742
41	20	71.4	663	2 BG127096	CO496608 G.h.fbr-s
42	20	71.4	683	7 CO496608	CO091583 GR Ra12C
43	20	71.4	688	7 CO091583	CW381543 f5b5001f0
44	20	71.4	751	10 CW381543	DU027161 7874 Toma
45	20	71.4	788	10 DU027161	

ALIGNMENTS

RESULT 1  
BX992195  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
ORIGIN  
Query Match  
Best Local Similarity  
Matches  
DB

Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP232j24, genomic survey sequence.  
BX992195.1 GI:49723653  
GSS; genome survey sequence; MICEP.  
Mus musculus  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 540)  
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.  
Direct Submission  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER  
Location/Qualifiers  
1..540  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHP232j24"  
/clone\_lib="MHP"  
79.3%; Score 22.2; DB 10; Length 540;  
88.9%; Pred. No. 2.4e+02;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
1 CACATGTAACACAGACTTCATTTGG 27  
275 CACATGTAGCACAGACTGCATTTGG 301

CNS03C2M  
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 013B17 of library G from tetraodon nigroviridis, genomic survey sequence.  
AL237271





```

Query Match      77.1%; Score 21.6; DB 9; Length 1128;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAGACTTCATTTCG 28
    312 CACTGTAAAGACATGACTTCATTTCG 285

Db
RESULT 5
CO646793
LOCUS
DEFINITION
ILLUMIGEN MCQ_39642 Katze MMPB2 Macaca mulatta cDNA clone
IBUW:22782 5' similar to Bases 5 to 734 highly similar to human
WDR36 (Hs.175596), mRNA sequence.
ACCESSION
CO646793
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE
1 (bases 1 to 834)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
TITLE
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL
Genome Biol. 6 (7), R60 (2005)
PUBMED
15998449
COMMENT
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.27. 681 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCCTCACTAAAGGGACAAA
BACKWARD: CACTATAGGCGGATTCGGTA
Insert Length: 834 Std Error: 0.00
Plate: CL000217 row: D column: 05
Seq primer: CCCTCACTAAAGGGACAAA
POLYA=No.
FEATURES
source
Location/Qualifiers
1..834
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBUW:22782"
/sex="male"
/tissue_type="blood"
/cell_type="PBMC"
/lab_stage="adult"
/dev_stage="adult"
/clone_lib="Katze MMPB2"
/clone="Vector: pDONR 222; Site 1: BarG I; Site 2: BarG I;
Created from CloneMiner cDNA Library Construction kit
(catalog #18249-029)"
ORIGIN
Query Match      75.7%; Score 21.2; DB 7; Length 834;
Best Local Similarity 88.5%; Pred. No. 6.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CACATGTAATAACAGACTTCATTTCG 26
    312 CACTGTAAAGACATGACTTCATTTCG 285

Db
RESULT 6
CO646661/c
LOCUS
DEFINITION
Schmidtea mediterranea clone H.25.6h unknown mRNA sequence.
ACCESSION
AY066661
VERSION
AY066661.1 GI:24796201
KEYWORDS
HTC.
SOURCE
Schmidtea mediterranea
ORGANISM
Schmidtea mediterranea
Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriate;
Tricladida; Paludicola; Dugesidae; Schmidtea.
REFERENCE
1 (bases 1 to 942)
Alvarado,A.S., Newmark,P.A., Robb,S.M.C. and Juste,R.B.
TITLE
The Schmidtea mediterranea database as a molecular resource for
studying platyhelminthes, stem cells and regeneration
JOURNAL
Development 129 (24), 5659-5665 (2002)
PUBMED
12421706
REFERENCE
2 (bases 1 to 942)
Alvarado,A.S., Newmark,P.A., Juste,R.B. and Robb,S.M.C.
AUTHORS
Direct Submission
TITLE
Submitted (07-DEC-2001) Neurobiology & Anatomy, University of Utah
JOURNAL
School of Medicine, 50 North Medical Drive, Salt Lake City, UT
84132, USA
COMMENT
Clone names suffixed with 'T3' were sequenced from their 5' ends.
All other clones were obtained by sequencing from their 3' ends.
More details and other relevant information can be found at
http://planaria.neuro.utah.edu.
FEATURES
source
Location/Qualifiers
1..942
/organism="Schmidtea mediterranea"
/mol_type="mRNA"
/strain="CIW4"
/db_xref="taxon:79327"
/clone="H.25.6h"
1..942
/misc_feature
/Note="similar to (BC004070) Unknown (protein for
MGC:8213) Mus musculus"
ORIGIN
Query Match      75.7%; Score 21.2; DB 4; Length 942;
Best Local Similarity 88.5%; Pred. No. 6.6e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACATGTAATAACAGACTTCATTTCG 27
    399 AAATGAAACACAGACTTCATTTCG 374

Db
RESULT 7
BE581909
LOCUS
DEFINITION
kg56c05.y1 TEN95TM-SSR Strongyloides stercoralis cDNA 5' similar to
WP.Y113G7A.11 CE23282 , mRNA sequence.
ACCESSION
BE581909
VERSION
BE581909.1 GI:9832851
KEYWORDS
EST.
SOURCE
Strongyloides stercoralis
ORGANISM
Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloidea; Strongyloides.
REFERENCE
1 (bases 1 to 464)
McCartier,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarisvilli,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
TITLE
Unpublished (1999)
JOURNAL

```

## COMMENT

Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutman@nih.gov). DNA sequencing by: Washington University Genome Sequencing Center St. Louis.  
High quality sequence stop: 262.

## FEATURES

source

1..464  
Location/Qualifiers  
/organism="Strongyloides stercoralis"  
/mol\_type="mRNA"  
/strain="Rhabditiform larvae obtained from gerbils"  
/db\_xref="taxon:6248"  
/lab\_host="XL-1 Blue MRP" (Stratagene)"  
/clone\_lib="TM95TM-SSR"  
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1: EcoRI; Site 2: XhoI; mRNA was purified from 2 x 10E3 rhabditiform larvae which had been isolated from gerbils experimentally infected with larvae originally isolated from experimentally infected dogs. cDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the EcoRI site to the XhoI site. The library has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-1700)."

## ORIGIN

Query Match 74.3%; Score 20.8; DB 2; Length 464;  
Best Local Similarity 91.7%; Pred. No. 8.7e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ATGTAAACACAGACTTCATTTGG 27

DB 109 ATGGAACACAGACTTCCTTTGG 132

## RESULT 8

BX199941/c  
LOCUS BX199941  
DEFINITION Danio rerio genomic clone DK8Y-208J5, genomic survey sequence.  
ACCESSION BX199941  
VERSION BX199941.1 GI:28031827  
KEYWORDS GSS  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

## REFERENCE

1 (bases 1 to 642)  
Humphray, S.J., Huckle, E. and Durham, J.L.  
Direct Submission  
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphrey@sanger.ac.uk Unpublished

## AUTHORS

TITLE This sequence was generated from the T7 end of BAC 208J5. 208J5 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:  
JOURNAL http://www.sanger.ac.uk/Projects/D\_rerio/  
LOCATION/Qualifiers

## FEATURES

source

1..642  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone\_xref="DK8Y-208J5"  
/tissue\_type="Testis"  
/note="vector pIndigoBAC-536"

## ORIGIN

Query Match 74.3%; Score 20.8; DB 10; Length 642;  
Best Local Similarity 91.7%; Pred. No. 9.1e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAAACACAGACTTCATTT 24

DB 308 CACATGTAAACACAGACTTCATTT 285

## RESULT 9

CE147952/c  
LOCUS CE147952  
DEFINITION tigr-gss-dog-17000371304927 Dog Library Canis familiaris genomic, genomic survey sequence.  
ACCESSION CE147952  
VERSION CE147952.1 GI:35264744  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

1 (bases 1 to 652)  
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

## FEATURES

source

1..652  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

## ORIGIN

Query Match 74.3%; Score 20.8; DB 9; Length 652;  
Best Local Similarity 91.7%; Pred. No. 9.1e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ATGTAAACACAGACTTCATTTGG 27

DB 309 ATGAAACACAGACTTAATTTGG 286

## RESULT 10

BH341834  
LOCUS BH341834  
DEFINITION CH230-64E10.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-64E10, genomic survey sequence.  
ACCESSION BH341834  
VERSION BH341834.1 GI:17272568  
KEYWORDS GSS.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

1 (bases 1 to 546)  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartabeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,

```

Seq primer: SP6
High quality sequence stop: 477.
Location/Qualifiers
1. .576
/organism="Hemarus americanus"
/mol_type="mRNA"
/db_xref="taxon:6706"
/clone="Ha_mx0.53e01"
/tissue_type="gill, epipodite, branchiostegite, heart,
ovary, testis, antennal gland, abdominal muscle,
hepatopancreas, brain"
/dev_stage="Adult intermolt"
/clone_lib="Lobster Multiple Tissues, Normalized"
/notes="Vector: PCMV Sport 6.1; Total RNA samples were
prepared individually from each tissue, checked for
quality, then pooled for construction and normalization
of cDNA library by Invitrogen. Plasmids were isolated
and inserts end-sequenced by the Marine DNA Sequencing and
Analysis Facility at Mount Desert Island Biological
Laboratory. Traces were processed for submission to
dbEST by trace4dbest software (Parkinson, Anthony and
Blaxter, unpublished software)."
```

ORIGIN

Query Match	73.6%;	Score 20.6;	DB 7;	Length 576;
Best Local Similarity	85.2%;	Pred. No. 1.1e+03;		
Matches 23;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

```

QY      1  CACATGTAAACAAGACTTCATTTTGG  27
        |||||  |||  |||||  |||||  |||||
DB      63  CACATACCAAGAAGACTTCATTTTGG  37
```

RESULT 12	598 bp	mRNA	linear	EST 21-MAY-2004
EX859292	AGENAE	Rainbow trout	normalized testis library (ccbl)	
LOCUS	Oncorhynchus mykiss	CDNA clone tcbl001ld.p.11	5prim, mRNA sequence.	
DEFINITION	EX859292			
ACCESSION	EX859292.2	GI:42756060		
VERSION				
KEYWORDS	EST.			
SOURCE	Oncorhynchus mykiss (rainbow trout)			

```

ORGANISM
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 598)
Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Dec 16, 2003 this sequence version replaced gi:39956980.
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jeu.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0011 row: p column: 11
Seq primer: M13R.
Location/Qualifiers
1..598
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcbi001ld.p.11"
/tissue_type="testis"
/lab_host="DH10B"
/clone_lib="AGENAE Rainbow trout normalized testis library
(tcbl)"
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

```

/note="Vector: pTTT3D-pac; Clone distribution : AGENAE Resource centre, Francois PIUMI, Francois.Plumiojony.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

## ORIGIN

Query Match 73.6%; Score 20.6; DB 5; Length 598;  
Best Local Similarity 85.2%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACATGTAAACAGACTTCATTTCGC 28

Db 550 ACATGCAAGACAGACATCATTTTGC 576

## RESULT 13

CR033848

## LOCUS

DEFINITION 659 bp DNA linear GSS 05-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone WHPP232123, genomic survey sequence.

## ACCESSION

CR033848

## VERSION

GSS; genome survey sequence; MICR.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 659)

Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.

Direct Submission

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICR

## FEATURES

source

1..659

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/clone="WHPP232123"

/clone\_lib="WHPP"

## ORIGIN

Query Match 73.6%; Score 20.6; DB 11; Length 659;

Best Local Similarity 85.2%; Pred. No. 1.1e+03;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACATGTAAACAGACTTCATTTCGG 27

Db 275 CACATGTAGCAGGACTGCATTTCGG 301

## RESULT 14

CN949957/c

## LOCUS

DEFINITION 725 bp mRNA linear EST 08-JUN-2004

Ha\_mx0 27a03 SP6 Lobster Multiple Tissues, Normalized Homarus

americanus cDNA clone Ha\_mx0 27a03 5' similar to ref|XP\_309809.1|

ENSANGP0000018221 - Anopheles gambiae. Score = 251 bits (641),

Expect = 1e-65, mRNA sequence.

CN949957

CN949957.1 GI:48431547

EST.

Homarus americanus (American lobster)

Homarus americanus

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropidae; Homarus.

1 (bases 1 to 725)

Towle,D.W. and Smith,C.M.

Expressed sequence tags in a normalized cDNA library prepared from

## JOURNAL

## COMMENT

multiple tissues of adult intermolt American lobster, Homarus americanus  
Unpublished (2004)  
Contact: David W. Towle  
Marine DNA Sequencing and Analysis Center  
Mount Desert Island Biological Laboratory  
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA  
Tel: 207-288-9880 x474  
Fax: 207-288-2130  
Email: dtowle@mdibl.org  
Plate: 27 row: a column: 03  
Seq primer: SP6  
High quality sequence stop: 501.

## FEATURES

source

Location/Qualifiers

1..725

/organism="Homarus americanus"

/mol\_type="mRNA"

/db\_xref="taxon:6706"

/clone="Ha\_mx0 27a03"

/tissue\_type="Gill, epipodite, branchiostegite, heart,

ovary, testis, antennal gland, abdominal muscle,

hepatopancreas, brain"

/dev\_stages="Adult intermolt"

/note="Vector: pCMV Sport 6.1; Total RNA samples were

prepared individually from each tissue, checked for

quality, then pooled for construction and normalization

of cDNA library by Invitrogen. Plasmids were isolated

and inserts end-sequenced by the Marine DNA Sequencing and

Analysis Facility at Mount Desert Island Biological

Laboratory. Traces were processed for submission to

dbEST by trace2dbest software (Parkinson, Anthony and

Blaxter, unpublished software)."

## ORIGIN

Query Match 73.6%; Score 20.6; DB 7; Length 725;

Best Local Similarity 85.2%; Pred. No. 1.1e+03;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACATGTAAACAGACTTCATTTCGG 27

Db 73 CACATACCACAGAGACTTCATTTCGG 47

## RESULT 15

BZ462328/c

## LOCUS

DEFINITION 759 bp DNA linear GSS 13-DEC-2002

BOOAA76TR BO 1.6.2 KB tot Brassica oleracea genomic clone BOOAA76,

genomic survey sequence.

ACCESSION BZ462328

VERSION BZ462328.1 GI:26746914

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 759)

Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,

Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.

Whole genome shotgun sequencing of Brassica oleracea and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

15805490

Other GSSs: BOOAA76TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

## ORIGIN

**Qy**            1 CACATGTAAAAA CAAGACTTCATTTTGG 27  
               ||| ||| ||| ||| ||| ||| ||| |||  
**Db**            567 CAAATCTACATCAAGACTTCATTTTGG 541

Search completed: February 14, 2006, 05:30:03  
Job time : 1928 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2006, 23:57:57 ; Search time 96 Seconds  
(without alignments)  
518.455 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAAACAAGACTTCATTGTCG 28

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgm2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgm2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgm2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgm2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgm2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgm2\_6/ptodata/1/ina/PCUTUS COMB.seq.\*  
7: /cgm2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgm2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgm2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	2	US-07-988-430-61
2	28	100.0	28	2	US-08-425-336-59
3	28	100.0	28	2	US-08-488-113B-59
4	28	100.0	28	2	US-08-477-484B-59
5	28	100.0	28	2	US-08-646-360-59
6	28	100.0	28	3	US-08-839-765-59
7	28	100.0	28	3	US-09-136-389-59
8	28	100.0	28	3	US-09-610-838-59
9	28	100.0	28	3	US-09-711-485-59
10	28	100.0	28	6	PCT-US92-09487-61
11	24.8	88.6	813	2	US-07-901-707-11
12	24.8	88.6	813	2	US-07-901-707-57
13	24.8	88.6	813	2	US-07-988-430-11
14	24.8	88.6	813	2	US-07-988-430-57
15	24.8	88.6	813	2	US-08-425-336-11
16	24.8	88.6	813	2	US-08-488-113B-11
17	24.8	88.6	813	2	US-08-477-484B-11
18	24.8	88.6	813	2	US-08-646-360-11
19	24.8	88.6	813	2	US-08-621-803-246
20	24.8	88.6	813	3	US-08-839-765-11
21	24.8	88.6	813	3	US-09-136-389-11
22	24.8	88.6	813	3	US-09-217-352-246
23	24.8	88.6	813	3	US-09-610-838-11
24	24.8	88.6	813	3	US-09-711-485-11

25	24.8	88.6	813	6	PCT-US92-09487-11	Sequence 11, Appl
26	24.8	88.6	813	6	PCT-US92-09487-57	Sequence 57, Appl
27	24.8	88.6	955	2	US-08-621-803-258	Sequence 258, App
28	24.8	88.6	955	3	US-09-217-352-258	Sequence 258, App
29	24.8	88.6	1003	2	US-08-621-803-252	Sequence 252, App
30	24.8	88.6	1003	2	US-09-217-352-252	Sequence 252, App
31	24.8	88.6	1072	2	US-08-621-803-250	Sequence 250, App
32	24.8	88.6	1072	3	US-09-217-352-250	Sequence 250, App
33	20.2	72.1	2187	3	US-08-956-171E-329	Sequence 329, App
34	20.2	72.1	2187	3	US-08-781-986A-329	Sequence 329, App
35	20	71.4	11298	2	US-07-869-933-31	Sequence 31, Appl
36	20	71.4	11298	2	US-08-201-879A-2	Sequence 2, Appl
37	20	71.4	11298	3	US-08-103-663-31	Sequence 31, Appl
38	20	71.4	98567	3	US-09-949-016-11750	Sequence 11750, A
39	20	71.4	100567	3	US-09-949-016-16934	Sequence 16934, A
40	19.6	70.0	2100	2	US-09-771-161A-45	Sequence 45, Appl
41	19.6	70.0	3132	2	US-08-167-919A-9	Sequence 9, Appl
42	19.6	70.0	3132	3	US-08-715-106-9	Sequence 9, Appl
43	19.6	70.0	3132	3	US-09-442-649-9	Sequence 9, Appl
C 44	19.6	70.0	126982	3	US-09-949-016-16597	Sequence 16597, A
C 45	19.4	69.3	36	2	US-07-988-430-62	Sequence 62, Appl

## ALIGNMENTS

### RESULT 1

US-07-988-430-61  
; Sequence 61, Application US/07988430  
; Patent No. 5416202  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,430  
; FILING DATE: 19921209  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5416202and, Greta E.  
; REGISTRATION NUMBER: 35302  
; REFERENCE/DOCKET NUMBER: 31133  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 28 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-07-988-430-61

Query Match 100.0%; Score 28; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTTGGC 28

Db 1 CACATGTAACAAGACTTCATTTTGGC 28

## RESULT 2

US-08-425-336-59  
; Sequence 59, Application US/08425336  
; Patent No. 5621083  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/425,336  
; FILING DATE: 18-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Thomas C.  
; REGISTRATION NUMBER: P-36,989  
; REFERENCE/DOCKET NUMBER: 31394  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-425-336-59

Query Match 100.0%; Score 28; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTTGGC 28

Db 1 CACATGTAACAAGACTTCATTTTGGC 28

## RESULT 3

US-08-488-113B-59  
; Sequence 59, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-488-113B-59

Query Match 100.0%; Score 28; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTTTGGC 28

Db 1 CACATGTAACAAGACTTCATTTTGGC 28

## RESULT 4



US-08-477-484B-59  
; Sequence 59, Application US/08477484B  
; Patent No. 5756699  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,484B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-477-484B-59

Query Match 100.0%; Score 28; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28  
DB 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 5  
US-08-646-360-59  
; Sequence 59, Application US/08646360  
; Patent No. 5837491  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-646-360-59

Query Match 100.0%; Score 28; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAGACTTCATTGGC 28  
DB 1 CACATGTAACAAGACTTCATTGGC 28

RESULT 6  
US-08-839-765-59  
; Sequence 59, Application US/08839765  
; Patent No. 6146631  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
;; STREET: 500 West Madison Street, 34th floor  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60661  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/839,765  
;; FILING DATE: 15-APR-1997  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/425,336  
;; FILING DATE: 18-APR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/064,691  
;; FILING DATE: 12-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/988,430  
;; FILING DATE: 09-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 59:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-839-765-59

Query Match 100.0%; Score 28; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAACAGACTTCATTTTGGC 28  
Db 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 7  
US-09-136-389-59  
; Sequence 59, Application US/09136389  
; Patent No. 6146850  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; PROTEINS  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois

;; COUNTRY: USA  
;; ZIP: 60661  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/136,389  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/646,360  
;; FILING DATE: 13-MAY-1996  
;; APPLICATION NUMBER: PCT/US94/05348  
;; FILING DATE: 12-MAY-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/064,691  
;; FILING DATE: 12-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/988,430  
;; FILING DATE: 09-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/901,707  
;; FILING DATE: 19-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/787,567  
;; FILING DATE: 04-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McNicholas, Janet M.  
;; REGISTRATION NUMBER: 32,918  
;; REFERENCE/DOCKET NUMBER: 200-70.P4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/707-8889  
;; TELEFAX: 312/707-9155  
;; TELEX: 650 388-1248  
;; INFORMATION FOR SEQ ID NO: 59:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-09-136-389-59

Query Match 100.0%; Score 28; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAACAGACTTCATTTTGGC 28  
Db 1 CACATGTAACAAACAGACTTCATTTTGGC 28

RESULT 8  
US-09-610-838-59  
; Sequence 59, Application US/09610838  
; Patent No. 6376217  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; PROTEINS  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,838  
FILING DATE: 06-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 09/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-610-838-59

Query Match 100.0%; Score 28; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTTTGGC 28  
|||  
Db 1 CACATGTAACAAGACTTCATTTTGGC 28

RESULT 9  
US-09-711-485-59  
; Sequence 59, Application US/09711485  
; Patent No. 6649742  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Heid & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-711-485-59

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Query Match      100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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**Qy** 1 CACATGTAACAAGACTTCATTTTGGC 28  
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**D6** 1 CACATGTAACAAGACTTCATTTTGGC 28  
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## RESULT 10

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PCT-US92-09487-61
; Sequence 61, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen P.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/09487  
FILING DATE: 19921104  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
PCT-US92-09487-61

Query Match 100.0%; Score 28; DB 6; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTTGGC 28  
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DB 1 CACATGTAACAAAGACTTCATTTTGGC 28

RESULT 11  
US-07-901-707-11  
Sequence 11, Application US/07901707  
Patent No. 5376546  
GENERAL INFORMATION:  
APPLICANT: Bernhardt, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Steve P.  
APPLICANT: Lane, Julie A.  
TITLE OF INVENTION: Materials Comprising and Methods of  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,707  
FILING DATE: 19920619  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5376546and, Greta E.  
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27129/30910  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-5750  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 813 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-07-901-707-11  
Query Match 88.6%; Score 24.8; DB 2; Length 813;  
Best Local Similarity 92.9%; Pred. No. 0.19;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACATGTAACAAAGACTTCATTTTGGC 28  
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DB 303 CACATGTAACAAAGACTTCATTTTGGC 330  
RESULT 12  
US-07-901-707-57  
Sequence 57, Application US/07901707  
Patent No. 5376546  
GENERAL INFORMATION:  
APPLICANT: Bernhardt, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Steve P.  
APPLICANT: Lane, Julie A.  
TITLE OF INVENTION: Materials Comprising and Methods of  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/901,707  
FILING DATE: 19920619  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5376546and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27129/30910  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-5750  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 813 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-07-901-707-57

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Query Match      88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CACATGTAATAACAAGACTTCATTCTTTGGC 28
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DB     303 CACAATAAATAACAAGACTTCATTCTTTGGC 330

RESULT 13
US-07-988-430-11
; Sequence 11, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; METHOD OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-988-430-11

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Query Match      88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CACATGTAACAAGACTTCATTTTGGC 28
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Db 303 CACATTTAAACAAGACTTCATTTTGGC 330

RESULT 14

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US-07-988-430-57
; Sequence 57, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Protein
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-988-430-57

Query Match 88.6%; Score 24.8; DB 2; Length 813;
Best Local Similarity 92.9%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CACATGTTAAACAAGACTTCATTGGC 28
Db 303 CACATTTAAACAAGACTTCATTGGC 330

RESULT 15
US-08-425-336-11
; Sequence 11, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140

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;;  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/425,336  
; FILING DATE: 18-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Thomas C.  
; REGISTRATION NUMBER: P-36,989  
; REFERENCE/DOCKET NUMBER: 31394  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 813 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-425-336-11

Query Match 88.6%; Score 24.8; DB 2; Length 813;  
Best Local Similarity 92.9%; Pred.No. 0.19; Mismatches 2; Indels 0; Gaps 0;  
Matches 26; Conservative 0;

QY 1 CACATGTAAACAAGACTTCATTTTGGC 28  
||| ||||| ||||| ||||| |||||  
Db 303 CACAATTAACAAGACTTCATTTTGGC 330

Search completed: February 13, 2006, 00:03:57  
Job time : 97 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2006, 00:55:33 ; Search time 424 Seconds  
(without alignments)  
546.091 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 28

Sequence: 1 CACATGTAACACAGCTTCATTGTCG 28

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA\_Main:\*  
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2: /cgm2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgm2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
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10: /cgm2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	28	100.0	28	9	US-10-717-243-59
3	24.8	88.6	813	3	US-09-765-527-246
4	24.8	88.6	813	6	US-10-127-890-11
5	24.8	88.6	813	9	US-10-717-243-11
6	24.8	88.6	955	3	US-09-765-527-258
7	24.8	88.6	1003	3	US-09-765-527-252
8	24.8	88.6	1072	3	US-09-765-527-250
9	24.8	88.6	1176	6	US-10-074-596-2
10	24.8	88.6	1500	9	US-10-964-195-12
11	24.8	88.6	1527	6	US-10-074-596-10
12	24.8	88.6	2407	10	US-11-084-080-25
13	21.6	77.1	600	9	US-10-972-079-84211
14	21.6	77.1	600	9	US-10-972-079-84212
15	21.6	77.1	600	9	US-10-972-079-84213
16	21.6	77.1	600	9	US-10-972-079-84214
17	20.6	73.6	38142	8	US-10-417-375-55
18	20.2	72.1	2187	2	US-08-781-986A-329
19	20.2	72.1	2187	7	US-10-329-624-329
20	20	71.4	11298	3	US-09-960-706-705
21	19.8	70.7	349	7	US-10-424-599-12953
22	19.8	70.7	742	5	US-10-027-632-141533
23	19.8	70.7	742	5	US-10-027-632-141534

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C 25	19.8	70.7	742	6	US-10-027-632-141534	Sequence 141534,
C 26	19.8	70.7	13886	8	US-10-741-600-17592	Sequence 17592, A
C 27	19.6	70.0	553	4	US-09-925-065A-436767	Sequence 436767,
C 28	19.6	70.0	598	4	US-09-925-065A-391252	Sequence 391252,
C 29	19.6	70.0	2100	3	US-09-771-161A-45	Sequence 45, Appl
C 30	19.6	70.0	2793	9	US-10-794-514A-470	Sequence 470, Appl
C 31	19.6	70.0	2949	9	US-10-489-135B-12	Sequence 12, Appl
C 32	19.6	70.0	2952	6	US-10-345-680-3	Sequence 3, Appl
C 33	19.6	70.0	2953	7	US-10-384-339C-3	Sequence 3, Appl
C 34	19.6	70.0	3149	5	US-10-205-823-96	Sequence 96, Appl
C 35	19.6	70.0	3149	6	US-10-345-680-1	Sequence 1, Appl
C 36	19.6	70.0	3149	6	US-10-295-027-601	Sequence 601, Appl
C 37	19.6	70.0	3149	8	US-10-473-974-320	Sequence 220, Appl
C 38	19.6	70.0	3149	10	US-11-051-454-96	Sequence 96, Appl
C 39	19.6	70.0	5799	9	US-10-794-514A-468	Sequence 468, Appl
C 40	19.6	70.0	5835	8	US-10-723-860-6909	Sequence 6909, Ap
C 41	19.4	69.3	36	6	US-10-127-890-60	Sequence 60, Appl
C 42	19.4	69.3	36	9	US-10-717-243-60	Sequence 60, Appl
C 43	19.4	69.3	1223197	5	US-10-027-632-179264	Sequence 179264,
C 44	19.4	69.3	1223197	6	US-10-027-632-179264	Sequence 179264,
C 45	19.2	68.6	179	3	US-09-783-590-2798	Sequence 2798, Ap

ALIGNMENTS

RESULT 1

US-10-127-890-59  
; Sequence 59, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127,890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889

```
;
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-127-890-59

Query Match      100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CACATGTAACAAAGACTTCATTTGGC 28
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DB      1 CACATGTAACAAAGACTTCATTTGGC 28

RESULT 2
US-10-717-243-59
; Sequence 59, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
;           Carroll, Stephen F.
;           Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                     Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-717-243-59

Query Match      100.0%; Score 28; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CACATGTAACAAAGACTTCATTTGGC 28
      ||| ||| ||| ||| ||| ||| ||| |||
DB      1 CACATGTAACAAAGACTTCATTTGGC 28

RESULT 3
US-09-765-527-246
; Sequence 246, Application US/09765527
; Patent No. US2002000638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
;                     Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael P.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "gelonin"
; SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-765-527-246

Query Match      88.6%; Score 24.8; DB 3; Length 813;
Best Local Similarity 92.9%; Pred. No. 3;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CACATGTAACAAAGACTTCATTTGGC 28
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DB      303 CACAATTAACAAAGACTTCATTTGGC 330

RESULT 4
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; COUNTRY: United States of America
; ZIP: 60606-6402
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 258:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
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; FEATURE:
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; FEATURE:
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; OTHER INFORMATION: /label= EcoRI
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; B."
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; FEATURE:
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; OTHER INFORMATION: /label= pel B
; /note="pel B is the leader sequence from the pectate lyase
; gene of Erwinia caratovora."
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; NAME/KEY: misc feature
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; OTHER INFORMATION: /label= "gelonin"
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; LOCATION: AA 276-279
; OTHER INFORMATION: /label= cleavage linker
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; site."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 280-293
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; NAME/KEY: misc feature
; LOCATION: residues 945-954
; OTHER INFORMATION: /label= XhoI
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; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-09-765-527-258
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Query Match      88.6%; Score 24.8; DB 3; Length 955;
Best Local Similarity 92.9%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACATGTAACAAAGACTTCATTTTGGC 28
    |||||
DB 434 CACATTAACAAAGACTTCATTTTGGC 461

RESULT 7
US-09-765-527-252
; Sequence 252, Application US/09765527
; Patent No. US20020006638A1
;
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
;
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 252:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..992
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: residues 1-65
; OTHER INFORMATION: /label= EcoRI
; /note="residues 1-65 comprise EcoRI site to beginning of pel
; B."
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: AA 1-22
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; /note="pel B is the leader sequence from the pectate lyase
; gene of Erwinia caratovora."
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; FEATURE:
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; LOCATION: AA 23-273
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; /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
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; /note="residues 993-1003 comprise stop codon and XhoI site."
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; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-09-765-527-252

Query Match      88.6%; Score 24.8; DB 3; Length 1003;
Best Local Similarity 92.9%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CACATGTAACAAGACTTCATTTCGC 28
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Db      434  CACAATTAACAAGACTTCATTTCGC 461

RESULT 8
US-09-765-527-250
; Sequence 250, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/765,527
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; B."
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; gene of Erwinia caratovora."
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; /note="EagI cloning site."
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; OTHER INFORMATION: /label= SLT linker
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; NAME/KEY: misc feature
; LOCATION: AA 297-298
; OTHER INFORMATION: /label= FspI/ScaI
; /note="FspI and ScaI cloning sites."
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; OTHER INFORMATION: /label= XhoI
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; SEQUENCE DESCRIPTION: SEQ ID NO: 250:
US-09-765-527-250

Query Match      88.6%; Score 24.8; DB 3; Length 1072;
Best Local Similarity 92.9%; Pred. No. 3.2;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CACATGTAACAAGACTTCATTTCGC 28
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Db      434  CACAATTAACAAGACTTCATTTCGC 461

RESULT 9
US-10-074-596-2
; Sequence 2, Application US/10074596
; Publication No. US2003017633A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; MAKING THEREOF
; FILE REFERENCE: CLFR:007US
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Query Match 77.1%; Score 21.6; DB 9; Length 600;  
Best Local Similarity 85.7%; Pred. No. 63;

matches 24; conservative 0; mismatches 4; indels 0; gaps 0  
 1 CACATGTAAAAACAAGACTTCATTTGGC 28

Db 211 CACTTGTAGACATGACTTCATTTTGAC 238

Search completed: February 13, 2006, 01:05:13  
Job time : 425 secs

Query Match 77.1%; Score 21.6; DB 9; Length 600;  
Best Local Similarity 85.7%; Pred. No. 63;  
Matches 24; Conservative 0; Mismatches 4; Indels

**Qy**      1    CACATGTAATAACAAGACTTCATTTGGC 28  
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**Dd**     303 CACTTGTAAGACATGACTTCATTTGAC 330

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RESULT 15
; Sequence 84213, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFIELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	19.8	70.7	2229	7	US-10-750-185-61204	Sequence 61204, A
2	19.8	70.7	2229	7	US-10-750-623-61204	Sequence 61204, A
3	19.4	69.3	172147	11	US-11-112-908-22	Sequence 22, Appl
4	19.4	69.3	212805	11	US-11-112-908-19	Sequence 19, Appl
5	19	67.9	1706	6	US-10-517-451-5	Sequence 5, Appl
6	19	67.9	1730	7	US-10-131-826-7	Sequence 7, Appl
7	19	67.9	1770	7	US-10-750-185-35041	Sequence 35041, A
8	19	67.9	1770	7	US-10-750-623-35041	Sequence 35041, A
9	18.8	67.1	50	11	US-11-175-859-30235	Sequence 30235, A
10	18.8	67.1	150038	11	US-11-121-086-23	Sequence 23, Appl
11	18.6	66.4	2166	7	US-10-750-185-56714	Sequence 56714, A
12	18.6	66.4	2166	7	US-10-750-623-56714	Sequence 56714, A
13	18.6	66.4	3829	7	US-10-821-234-289	Sequence 289, App
14	18.4	65.7	2007	7	US-10-750-185-59158	Sequence 59158, A
15	18.4	65.7	2007	7	US-10-750-623-59158	Sequence 59158, A
16	18	64.3	600	11	US-11-136-527-6304	Sequence 6304, Ap
17	18	64.3	894	7	US-10-750-185-49301	Sequence 49301, A
18	18	64.3	894	7	US-10-750-623-49301	Sequence 49301, A
19	18	64.3	1021	11	US-11-128-061-392	Sequence 392, App
20	18	64.3	1021	11	US-11-128-061-4034	Sequence 4034, App
21	18	64.3	1021	11	US-11-128-049-392	Sequence 392, App

```
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61204
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Bovine 19866880972028
US-10-750-623-61204

Query Match          70.7%; Score 19.8; DB 7; Length 17229;
Best Local Similarity 91.3%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTAAACAAGACTTCATTGGC 28
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Db 1332 GTAAACAAGAAATTCATTGGAC 1354

RESULT 3
US-11-112-908-22
; Sequence 22, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 172147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-22

Query Match          69.3%; Score 19.4; DB 11; Length 172147;
Best Local Similarity 95.2%; Pred. No. 73;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 AAAACAAGACTTCATTGGC 28
   ||||| ||||| ||||| ||||| |||||
Db 12427 AAAATAAGACTTCATTGGC 12447

RESULT 4
US-11-112-908-19
; Sequence 19, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
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; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 212805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-19

Query Match          69.3%; Score 19.4; DB 11; Length 212805;
Best Local Similarity 95.2%; Pred. No. 74;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 AAAACAAGACTTCATTGGC 28
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Db 173946 AAAATAAGACTTCATTGGC 173966

RESULT 5
US-10-517-151-5
; Sequence 5, Application US/10517151
; Publication No. US20060019252A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Oncotherapy Science, Inc.
; APPLICANT: The University of Tokyo
; TITLE OF INVENTION: Genes and Polypeptides Relating to Hepato cellular or
; FILE REFERENCE: 082379-000400US
; CURRENT APPLICATION NUMBER: US/10/517,151
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/386,985
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: WO PCT/JP03/07070
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (205)..(705)
; OTHER INFORMATION:
US-10-517-151-5

Query Match          67.9%; Score 19; DB 6; Length 1706;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ACATGTAAACAAGACTTCATTGGC 28
   ||||| ||||| ||||| ||||| |||||
Db 775 ACATGTAAATGCTAAATTCATTGGC 801

RESULT 6
US-10-131-826A-7
; Sequence 7, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
```



```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 7
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-7

Query Match      67.9%; Score 19; DB 7; Length 1730;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 0; Gaps 0;

Qy      2  ACATGTAACAAAGACTTCATTTGGC 28
Db      800 ACATGTAATGCTAATTTTCATTTGGC 826

RESULT 7
US-10-750-185-35041/c
; Sequence 35041, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 7
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-7

Query Match      67.9%; Score 19; DB 7; Length 1730;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 0; Gaps 0;

Qy      2  ACATGTAACAAAGACTTCATTTGGC 28
Db      800 ACATGTAATGCTAATTTTCATTTGGC 826

RESULT 7
US-10-750-185-35041/c
; Sequence 35041, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35041
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Bovine 19866880821523
US-10-750-623-35041/c

Query Match      67.9%; Score 19; DB 7; Length 1770;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CACATGTAACAAAGACTTCATTTGG 27
Db      416 CACATGTAACAAAGACTTCATTTGG 390

RESULT 8
US-10-750-623-35041/c
; Sequence 35041, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35041
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Bovine 19866880821523
US-10-750-623-35041

Query Match      67.9%; Score 19; DB 7; Length 1770;
Best Local Similarity 81.5%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CACATGTAACAAAGACTTCATTTGG 27
Db      416 CACATGTAACAAAGACTTCATTTGG 390

RESULT 9
US-11-175-859-30235/c
; Sequence 30235, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 118251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 30235
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-30235
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US-10-750-185-59158  
; Sequence 59158, Application US/10750185  
; Publication No. US20050260603A1

; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 59158  
; LENGTH: 2007  
; TYPE: DNA  
; ORGANISM: Bovine 19866881015410  
US-10-750-185-59158

Query Match 65.7%; Score 18.4; DB 7; Length 2007;  
Best Local Similarity 78.6%; Pred. No. 1.4e+02;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACATGTAAACAAGACTTCATTTGGC 28  
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Db 1535 CATGTGGAACAACAAGCTTCATTCCTGGC 1562

RESULT 15  
US-10-750-623-59158  
; Sequence 59158, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 59158  
; LENGTH: 2007  
; TYPE: DNA  
; ORGANISM: Bovine 19866881015410  
US-10-750-623-59158

Query Match 65.7%; Score 18.4; DB 7; Length 2007;  
Best Local Similarity 78.6%; Pred. No. 1.4e+02;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CACATGTAAACAAGACTTCATTTGGC 28  
||| ||||| ||||| ||||| |||||  
Db 1535 CATGTGGAACAACAAGCTTCATTCCTGGC 1562

Search completed: February 13, 2006, 01:08:51  
Job time : 213 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 09:56:49 ; Search time 136.614 Seconds  
(without alignments)  
807.265 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDVTVSSTGATVITYVNF.....AVDQVKIALLKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1980s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	251	2	AAR63914 Type I RI
2	1273	99.7	251	2	AAR63912 Type I RI
3	1269	99.4	251	2	AAR63903 Type I RI
4	1269	99.4	251	2	AAR63915 Type I RI
5	1269	99.4	251	8	ADG63044 Gelonium
6	1269	99.4	316	5	ABG71551 G. multif
7	1269	99.4	498	9	ABE68722 scFv23-ge
8	1269	99.4	507	5	ABG71552 Murine sc
9	1266	99.1	293	2	AAW29300 BPI pepti
10	1266	99.1	309	2	AAW29303 BPI pepti
11	1266	99.1	332	2	AAW29294 BPI pepti
12	1264	99.0	251	2	AAR63923 Type I RI
13	1261	98.7	251	2	AAR63921 Type I RI
14	1261	98.7	251	2	AAR63918 Type I RI
15	1261	98.7	251	2	AAR63920 Type I RI
16	1261	98.7	251	2	AAR63919 Type I RI
17	1261	98.7	251	2	AAR63924 Type I RI
18	1260	98.7	251	2	AAR63922 Type I RI
19	1260	98.7	251	2	AAR63916 Type I RI
20	1260	98.7	251	2	AAR63917 Type I RI
21	1257	98.4	251	2	AAR74177 Type I ri
22	1251	98.0	251	2	AAR37291 Plant typ
23	1235.5	96.8	258	2	AAR22227 Gelonin t
24	1201	94.0	506	9	ABE68720 scFv23-ge

25	1171	91.7	235	2	AAR63913	Aar63913 Type I RI
26	348	27.3	263	2	AAR63905	Aar63905 Type I RI
27	348	27.3	263	2	AAR74179	Aar74179 Type I ri
28	348	27.3	263	8	ADG63043	Adg63043 Momordica
29	347	27.2	565	1	AAP50166	Aap50166 Sequence
30	347	27.2	565	4	AAG78300	Aag78300 Castor be
31	347	27.2	574	1	AAP70325	Aap70325 Sequence
32	346	27.1	267	2	AAR30722	Aar30722 Ricin A f
33	346	27.1	267	2	AAR37290	Aar37290 Ricin A c
34	346	27.1	267	2	AAR63902	Aar63902 Ricin A-c
35	346	27.1	267	3	AB19265	Ab19265 Amino aci
36	346	27.1	267	7	ADC24288	Adc24288 Ricin tox
37	346	27.1	268	2	AAR39570	Aar39570 Sequence
38	346	27.1	290	2	AAW21699	Aaw21699 Ricin A-c
39	346	27.1	290	2	AAW25136	Aaw25136 Ricin A-c
40	346	27.1	332	1	AAP70097	Aap70097 Ricin A.
41	346	27.1	332	1	AAP70838	Aap70838 Sequence
42	346	27.1	332	1	AAP95639	Aap95639 Ricin A e
43	346	27.1	554	2	AAR70827	Aar70827 Anti-cata
44	346	27.1	562	1	AAP90079	Aap90079 Ricin D.
45	346	27.1	565	4	AAG78304	Aag78304 Modified

ALIGNMENTS

RESULT 1

AAR63914

ID AAR63914 standard; protein; 251 AA.

XX AC AAR63914;

XX AC

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX

DE Type I RIP gelonin analog Gel (A44/A50) .

XX Type I ribosome-inactivating proteins; RIPs; gelonin;

KW cytotoxic therapeutic agents; autoimmune disease; cancer;

KW graft-versus-host disease.

XX Gelonium multiflorum.

OS Gelonium multiflorum.

PN W09426910-A1.

XX

XX

PD 24-NOV-1994.

XX

PF 12-MAY-1994; 94WO-US005348.

XX

PR 12-MAY-1993; 93US-00064691.

XX (XOMA ) XOMA CORP.

XX

PI Better MD, Carroll SP, Studnicka GM;

XX

XX WPI; 1995-006804/01.

XX

PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which

FT are suitable for use as components of cytotoxic therapeutic agents.

XX

PS

XX Example 3; Page 181-182; 221pp; English.

XX

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating

CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.

CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which

CC include gene fusion products and immunocjugates. CTAs may be used to

CC selectively eliminate any cell type to which a RIP component is

CC targeted, by the specific binding capacity of the second component of

CC the agent. They can be used in the treatment of diseases where the

CC elimination of a particular cell type is desired, such as autoimmune

CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to

XX correct PN field.)

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SQ Sequence 251 AA;
Query Match 100.0%; Score 1277; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 4.9e-120;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITVYVNFLELNRVVKLPKGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGATYITVYVNFLELNRVVKLPKGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 QGLAEIAIDVTSVYVVGQVNRNRSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVVGQVNRNRSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 2
AAR63912
ID AAR63912 standard; protein; 251 AA.
XX
AC AAR63912;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I RIP gelonin analog Gel (A50/C44).
XX
KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
FN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 3; Page 179-180; 221pp; English.
XX
CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating
CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.
CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which
CC include gene fusion products and immunoconjugates. CTAs may be used to
CC selectively eliminate any cell type to which a RIP component is
CC targeted, by the specific binding capacity of the second component of
CC the agent. They can be used in the treatment of diseases where the
CC elimination of a particular cell type is desired, such as autoimmune
CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC correct FN field.)

SQ Sequence 251 AA;
Query Match 99.7%; Score 1273; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.2e-119;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDVSFSTKGATYITVYVNFLELNRVVKLPKGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
DB 1 GLDVSFSTKGATYITVYVNFLELNRVVKLPKGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
QY 61 QGLAEIAIDVTSVYVVGQVNRNRSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
DB 61 QGLAEIAIDVTSVYVVGQVNRNRSYFFPKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQVSEAAARFTFIENQIRNN 180
QY 181 FQORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
DB 181 FQORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240
QY 241 ALLKFVDKDPK 251
DB 241 ALLKFVDKDPK 251

RESULT 3
AAR63903
ID AAR63903 standard; protein; 251 AA.
XX
AC AAR63903;
XX
DT 25-MAR-2003 (revised)
DT 27-JUL-1995 (first entry)
XX
DE Type I ribosome-inactivating protein gelonin.
XX
KW Type I ribosome-inactivating proteins; RIPs; gelonin;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
OS Gelonium multiflorum.
XX
FN WO9426910-A1.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US005348.
XX
PR 12-MAY-1993; 93US-00064691.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Carroll SF, Studnicka GM;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT are suitable for use as components of cytotoxic therapeutic agents.
XX
PS Example 1; Fig 1; 221pp; English.
XX
CC AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP)
CC gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key
CC components of cytotoxic therapeutic agents (CTAs), which include gene
CC fusion products and immunoconjugates. CTAs may be used to selectively
CC eliminate any cell type to which a RIP component is targeted, by the
CC specific binding capacity of the second component of the agent. They can
CC be used in the treatment of diseases where the elimination of a
CC particular cell type is desired, such as autoimmune disease, cancer and
```

CC graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 251 AA;

Query Match 99.4%; Score 1269; DB 2; Length 251;  
 Best Local Similarity 99.2%; Pred. No. 3.1e-119; Mismatches 2; Indels 0; Gaps 0;  
 Matches 249; Conservative 0;  
 QY 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60  
 DB 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60  
 QY 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 DB 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 QY 121 AYRETTDGIPLRIGIKGLDENADNYKPTETIASLLVLIQWVSEARPTFIENQIRNN 180  
 DB 121 AYRETTDGIPLRIGIKGLDENADNYKPTETIASLLVLIQWVSEARPTFIENQIRNN 180  
 QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

## RESULT 4

AAR63915  
 ID AAR63915 standard; protein; 251 AA.

XX AAR63915;

XX 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)

XX Type I RIP gelonin analog Gel (C10/A44/A50).

XX Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA ) XOMA CORP.

XX Better MD, Carroll SF, Studnicka GW;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.

XX Example 3; Page 189-190; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune

CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

SQ Sequence 251 AA;

Query Match 99.4%; Score 1269; DB 2; Length 251;  
 Best Local Similarity 99.6%; Pred. No. 3.1e-119; Mismatches 1; Indels 0; Gaps 0;  
 Matches 250; Conservative 0;

QY 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60

DB 1 GLDVSFSTKGATYYVNFNLRLVKLPKPGNSHGIPLLRKADDPGKAFVLVALSNDN 60

QY 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

DB 61 QQLAEIAIDVTSVYVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

QY 121 AYRETTDGIPLRIGIKGLDENADNYKPTETIASLLVLIQWVSEARPTFIENQIRNN 180

DB 121 AYRETTDGIPLRIGIKGLDENADNYKPTETIASLLVLIQWVSEARPTFIENQIRNN 180

QY 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

DB 181 FQORIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251

DB 241 ALLKFVDKDPK 251

## RESULT 5

ADG63044

ID ADG63044 standard; protein; 251 AA.

XX ADG63044;

XX 11-MAR-2004 (first entry)

XX Gelonium anti-HIV protein 31kDa (GAP31).

XX anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;  
 KW GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.

XX Gelonium multiflorum.

XX US6652861-B1.

XX 25-NOV-2003.

XX 25-AUG-2000; 2000US-00645603.

XX 26-AUG-1999; 99US-0150885P.

XX (UYNY ) UNIV NEW YORK STATE.

XX Lee-Huang S;

XX WPI; 2004-050519/05.

XX New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and  
 PT antiviral activity, useful for treating human immunodeficiency virus  
 PT infection or tumor.

XX Example 1; SEQ ID NO 2; 22pp; English.

XX The invention describes an isolated peptide or polypeptide having an anti  
 CC -tumor and antiviral activity. Also described is a composition  
 CC comprising the isolated peptide or polypeptide, and a carrier, excipient  
 CC or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or  
 CC polypeptides. The peptide or polypeptide is useful for treating HIV  
 CC infection, and tumour. This is the amino acid sequence of Gelonium anti-  
 CC HIV protein 30kDa (MAP30).

```
SQ Sequence 251 AA;
Query Match 99.4%; Score 1269; DB 8; Length 251;
Best Local Similarity 99.2%; Pred. No. 3.1e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 60
DB 1 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 60

QY 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 120
DB 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQWVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQWVSEAAARFTFIENQIRNN 180

QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYYVTAVDQVKPKI 240
DB 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYYVTAVDQVKPKI 240

QY 241 ALLKFPVDKDPK 251
DB 241 ALLKFPVDKDPK 251

RESULT 6
ABG71551
ID ABG71551 standard; protein; 316 AA.
XX ABG71551;
AC
XX
XX
DT 08-JAN-2003 (first entry)
DE
DE G. multiflorum recombinant gelonin (rGel) toxin.
XX Modified protein; reduced antigenicity; modified toxin; gelonin;
KW designer toxin; immunotoxin; proteinaceous compound; cancer;
KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;
KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;
KW inflammatory disease; cardiovascular disease; diabetes;
KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;
KW cardiant; antidiabetic; virucide; protozoacide; fungicide; antibacterial;
KW recombinant gelonin; rGel.
XX
XX
OS Gelonium multiflorum.
XX
XX
XX WO200269886-A2.
XX
XX
PD 12-SEP-2002.
XX
XX
XX 12-FEB-2002; 2002WO-US004195.
XX
XX
XX 12-FEB-2001; 2001US-0268402P.
XX
XX (RERE-) RES DEV FOUND.
XX
XX Rosenblum MG, Cheung L;
XX
XX WPI; 2002-750431/81.
XX
XX N-PSDB; ABS56021.
XX
XX Generating a modified protein with reduced antigenicity for treating
PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region
PT antigenic in the first subject using antiserum from either the first or a
PT second subject.
XX
XX Claim 63; Page 169-170; 176pp; English.
PS
XX The present invention relates to a method of generating a modified
CC protein with reduced antigenicity while maintaining its biological
CC activity. The method comprises identifying a region of the protein that
```

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CC is antigenic in a first subject using antiserum from either the first
CC subject or a second subject of the same species as the first subject. In
CC particular the invention discloses modified toxin compounds, for example
CC gelonin toxin derived from Gelonium multiflorum, that are truncated
CC and/or possess reduced antigenicity. Such designer toxins have
CC therapeutic, diagnostic, and preventative benefits, particularly as
CC immunotoxins. The method of the invention is useful for generating
CC proteinaceous compounds with less antigenicity. The immunotoxin and
CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,
CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
CC compositions of the invention are also useful for treating microbial
CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
CC diseases, hyperproliferative disorders including cancer, leukaemias,
CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic
CC diseases, and diabetes. The method provides less antigenic proteins,
CC peptides and polypeptides, which are more effective than prior art. The
CC present sequence represents G. multiflorum recombinant gelonin (rGel)
XX
SQ Sequence 316 AA;
Query Match 99.4%; Score 1269; DB 5; Length 316;
Best Local Similarity 99.2%; Pred. No. 4.3e-119;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 60
DB 47 GLDTVSFSTKGATYTYVNFNLRLVKLPKGNHSHGIPLLRKKADDPKAPVLVALSNDN 106

QY 61 QQLAEIAIDVTSVYVGVQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 120
DB 107 QQLAEIAIDVTSVYVGVQVRNRSYFFKADAPDAAYEGLFKNTIKTRLHFGGSYPSLGEK 166

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQWVSEAAARFTFIENQIRNN 180
DB 167 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTIASSLLVVIQWVSEAAARFTFIENQIRNN 226

QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYYVTAVDQVKPKI 240
DB 227 FQQRIRPANNTISLENKWKGLSFQIRTSANGMPSEAVELERANGKKYYVTAVDQVKPKI 286

QY 241 ALLKFPVDKDPK 251
DB 287 ALLKFPVDKDPK 297

RESULT 7
AEB68722
ID AEB68722 standard; protein; 498 AA.
XX
XX AEB68722;
AC
XX
XX 06-OCT-2005 (first entry)
XX
XX scFv23-gelonin immunotoxin amino acid sequence SEQ ID NO:13.
DE
XX antibody engineering; c-erbB-2 protein; toxin; gelonin; cytostatic;
XX immunotoxin; neoplasm.
XX
XX Synthetic.
XX
XX US2005163774-A1.
XX
XX 28-JUL-2005.
XX
XX 13-OCT-2004; 2004US-00964195.
XX
XX 10-APR-1992; 92US-00867728.
XX
XX 09-DEC-1993; 93US-00164638.
XX
XX 02-SEP-1994; 94US-00300082.
XX
XX 17-MAR-1995; 95US-00404499.
XX
XX 26-MAY-1999; 99US-00320156.
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XX (RERE-) RES DEV FOUND.  
 XX Rosenblum M, Shawver LK;  
 XX WPI; 2005-561813/57.  
 XX N-PSDB; ABB68721.  
 XX New immunotoxins directed against c-erbB-2 related surface antigens,  
 PT useful for treating neoplastic diseases, e.g. carcinoma or  
 PT adenocarcinoma.  
 XX Disclosure; SEQ ID NO 13; 60pp; English.  
 XX The invention relates to a composition comprising a conjugate of an  
 CC antibody exhibiting binding specificity for an extracellular epitope of c  
 CC -erbB-2 protein and a plant derived toxin, where the toxin is  
 CC pharmacologically effective against neoplastic cells and is selected from  
 CC gelonin, full length recombinant gelonin, functional gelonin fragments or  
 CC functional gelonin derivatives. Also described is a pharmaceutical  
 CC composition comprising the composition above and a pharmaceutical  
 CC vehicle. For treating neoplastic diseases, e.g. human mammary carcinomas,  
 CC human ovarian carcinomas, lung carcinomas, gastric tumors, salivary gland  
 CC adenocarcinomas, or colon adenocarcinomas. The present sequence  
 CC represents a scFv23-gelonin amino acid sequence, which is used in an  
 CC example from the present invention.  
 XX  
 XX SQ Sequence 498 AA;  
 Query Match 99.4%; Score 1269; DB 9; Length 498;  
 Best Local Similarity 99.2%; Pred. No. 8.2e-119;  
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 60  
 DB 247 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 306  
 QY 61 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120  
 DB 307 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 366  
 QY 121 AYRTETDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEARFTFIENQIRNN 180  
 DB 367 AYRTETDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEARFTFIENQIRNN 426  
 QY 181 FQQRIRPANNNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 DB 427 FQQRIRPANNNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 486  
 QY 241 ALLKFVDKDPK 251  
 DB 487 ALLKFVDKDPK 497  
 RESULT 8  
 ABG71552  
 ID ABG71552 standard; protein; 507 AA.  
 XX  
 AC ABG71552;  
 XX  
 DT 08-JAN-2003 (first entry)  
 XX  
 DE Murine scfWML/G. multiflorum rGel fusion protein.  
 XX Modified protein; reduced antigenicity; modified toxin; gelonin;  
 KW designer toxin; immunotoxin; proteinaceous compound; cancer;  
 KW microbial pathogenesis; acquired immunodeficiency syndrome; AIDS;  
 KW autoimmune disease; hyperproliferative disorder; leukaemia; arthritis;  
 KW inflammatory disease; cardiovascular disease; diabetes;  
 KW pathogenic disease; cytostatic; antiarthritic; antiinflammatory;  
 KW murine; antidiabetic; virucide; proteoacide; fungicide; antibacterial;  
 KW murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;  
 KW scfWML/rGel; mutant; mutein.

XX Mus sp.  
 OS Gelonium multiflorum.  
 OS Synthetic.  
 OS Chimeric.  
 XX W0200269886-A2.  
 XX 12-SEP-2002.  
 XX 12-FEB-2002; 2002WO-US004195.  
 XX 12-FEB-2001; 2001US-0268402P.  
 XX (RERE-) RES DEV FOUND.  
 XX Rosenblum MG, Cheung L;  
 XX WPI; 2002-750431/81.  
 XX N-PSDB; ABS56029.  
 XX Generating a modified protein with reduced antigenicity for treating  
 PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region  
 PT antigenic in the first subject using antiserum from either the first or a  
 PT second subject.  
 XX  
 XX PS Disclosure; Page 174-176; 176pp; English.  
 XX The present invention relates to a method of generating a modified  
 CC protein with reduced antigenicity while maintaining its biological  
 CC activity. The method comprises identifying a region of the protein that  
 CC is antigenic in a first subject using antiserum from either the first  
 CC subject or a second subject of the same species as the first subject. In  
 CC particular the invention discloses modified toxin compounds, for example  
 CC gelonin toxin derived from Gelonium multiflorum, that are truncated  
 CC and/or possess reduced antigenicity. Such designer toxins have  
 CC therapeutic, diagnostic, and preventative benefits, particularly as  
 CC immunotoxins. The method of the invention is useful for generating  
 CC proteinaceous compounds with less antigenicity. The immunotoxin and  
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,  
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,  
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall  
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The  
 CC compositions of the invention are also useful for treating microbial  
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune  
 CC diseases, hyperproliferative disorders including cancer, leukemias,  
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic  
 CC peptides and polypeptides, which are more effective than prior art. The  
 CC present sequence represents murine single-chain ZME-018 antibody/G.  
 CC multiflorum recombinant gelonin (rGel) (scfWML/rGel) fusion protein  
 XX  
 XX SQ Sequence 507 AA;  
 Query Match 99.4%; Score 1269; DB 5; Length 507;  
 Best Local Similarity 99.2%; Pred. No. 8.4e-119;  
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 60  
 DB 257 GLDTVSFSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDN 316  
 QY 61 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120  
 DB 317 GQLAEIAIDVTSVYVGVQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 376  
 QY 121 AYRTETDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEARFTFIENQIRNN 180  
 DB 377 AYRTETDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEARFTFIENQIRNN 436  
 QY 181 FQQRIRPANNNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 DB 437 FQQRIRPANNNTISLENKWKLSFOIRTSGANGMFSEAVELERANGKYYVTVAVDQVKPKI 496

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Qy      241 ALLKFDVDDPK 251
Db      497 ALLKFDVDDPK 507

RESULT 9
AAW29300
ID      AAW29300 standard; protein; 293 AA.
XX
AC      AAW29300;
XX
DT      20-APR-1998 (first entry)
XX
DE      BPI peptide fusion protein PING3797 vector construct protein.
XX
KW      Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW      bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW      fungicidal; recombinant DNA; vector.
XX
OS      Synthetic.
OS      Pectobacterium carotovorum.
OS      Homo sapiens.
OS      Chimeric.
XX
FN      WO9735009-A1.
XX
PD      25-SEP-1997.
XX
PF      18-MAR-1997; 97WO-US005287.
XX
PR      22-MAR-1996; 96US-00621803.
XX
PA      (XOMA ) XOMA CORP.
XX
PI      Better MD;
XX
DR      WPI; 1997-480215/44.
XX
DR      N-PSDB; AAT86336.
XX
RE      Recombinant production of bactericidal/permeability increasing protein -
PT      by expression as a fusion protein in microbial host cells, then cleaving
PT      the BPI peptide from the carrier.
XX
PS      Example 1; Page 160-161; 186pp; English.
XX
CC      A new recombinant DNA vector construct has been developed which encodes a
CC      fusion protein and is suitable for introduction into a bacterial host.
CC      The vector comprises: (a) DNA encoding at least one cationic
CC      bactericidal/permeability increasing peptide (BPI); (b) DNA encoding a
CC      carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC      located between (a) and (b). The present sequence represents the protein
CC      from the PING3797 vector construct which codes for a BPI fusion protein.
CC      The peptides have many uses including the treatment of bacterial and
CC      fungal infections. BPI peptides also bind to endotoxins and heparin,
CC      neutralising their effects. The peptides have further been shown to
CC      inhibit angiogenesis (partly due to heparin-binding activity). The fusion
CC      proteins have been found to be expressed in large amounts without
CC      significant proteolysis, and in some cases are actually secreted from the
CC      host cells. This allows the indirect production of anti-microbial BPI
CC      peptides in microbial hosts
XX
SQ      Sequence 293 AA;

Query Match          99.1%; Score 1266; DB 2; Length 293;
Best Local Similarity 98.8%; Pred. No. 7,8e-119;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GLDVSFSTKATYITVNFNLRLVKLPKGNHGIPLLRKKADDPKAFVLVSLSDN 60
Db      23 GLDVSFSTKATYITVNFNLRLVKLPKGNHGIPLLRKKADDPKAFVLVSLSDN 82
Qy      61 GQLAEIADVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGYSLEGEK 120

```

Query Match 99.1%; Score 1266; DB 2; Length 309;  
Best Local Similarity 98.8%; Pred. No. 8.4e-119;  
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GLDTVSPSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDDPKGKAPVLVALSNDN 60  
DB 23 GLDTVSPSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDDPKGKAPVLVALSNDN 82  
QY 61 GOLAEIAIDVTSVVVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 120  
DB 83 GOLAEIAIDVTSVVVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 142  
QY 121 AYRETTDLGIEPLRIGIKLLENADNIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180  
DB 143 AYRETTDLGIEPLRIGIKLLENADNIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 202  
QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 203 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 262  
QY 241 ALLKFVDKDPK 251  
DB 263 ALLKFVDKDPK 273

## RESULT 11

AAW29294  
ID AAW29294 standard; protein; 332 AA.  
XX AAW29294;  
AC AAW29294;  
XX XX  
XX 20-APR-1998 (first entry)  
XX BPI peptide fusion protein PING3793 vector construct protein.  
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;  
KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;  
KW fungicidal; recombinant DNA; vector.  
XX Synthetic.  
OS Pectobacterium carotovorum.  
OS Homo sapiens.  
OS Chimeric.  
XX XX  
XX WO9735009-A1.  
XX XX  
XX 25-SEP-1997.  
XX 18-MAR-1997; 97WO-US005287.  
XX 22-MAR-1996; 96US-00621803.  
XX (XOMA ) XOMA CORP.  
XX Better MD;  
XX WPI; 1997-480215/44.  
XX N-PSDB; AAT86332.  
XX Recombinant production of bactericidal/permeability increasing protein -  
XX by expression as a fusion protein in microbial host cells, then cleaving  
XX the BPI peptide from the carrier.  
XX Example 1; Page 148-150; 186pp; English.

XX A new recombinant DNA vector construct has been developed which encodes a  
XX fusion protein and is suitable for introduction into a bacterial host.  
XX The vector comprises: (a) DNA encoding at least one cationic  
XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a  
XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site  
XX located between (a) and (b). The present sequence represents the protein  
XX from the PING3793 vector construct which codes for a BPI fusion protein.

CC The peptides have many uses including the treatment of bacterial and  
CC fungal infections. BPI peptides also bind to endotoxins and heparin,  
CC neutralising their effects. The peptides have further been shown to  
CC inhibit angiogenesis (partly due to heparin-binding activity). The fusion  
CC proteins have been found to be expressed in large amounts without  
CC significant proteolysis, and in some cases are actually secreted from the  
CC host cells. This allows the indirect production of anti-microbial BPI  
CC peptides in microbial hosts  
XX XX

SQ Sequence 332 AA;

Query Match 99.1%; Score 1266; DB 2; Length 332;  
Best Local Similarity 98.8%; Pred. No. 9.3e-119;  
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTVSPSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDDPKGKAPVLVALSNDN 60  
DB 23 GLDTVSPSTKGATITTYVNFNLRLVKLPKGNHSHGIPLLRKKADDDPKGKAPVLVALSNDN 82  
QY 61 GOLAEIAIDVTSVVVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 120  
DB 83 GOLAEIAIDVTSVVVVGQVNRNSYFFPKADPAAYEGLFKNTIKTRLHFGGTSYPSLEGEK 142  
QY 121 AYRETTDLGIEPLRIGIKLLENADNIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 180  
DB 143 AYRETTDLGIEPLRIGIKLLENADNIDNYKPTETIASLLVVIQWVSEARFTFIENQIRNN 202  
QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 203 FQQRIRPANNTISLENKWKGLSFQIRTSANGMSEAVELERANGKYYVTVAVDQVKPKI 262  
QY 241 ALLKFVDKDPK 251  
DB 263 ALLKFVDKDPK 273

## RESULT 12

AAAR63923  
ID AAR63923 standard; protein; 251 AA.  
XX AAR63923;  
XX AC  
XX 25-MAR-2003 (revised)  
DT 27-JUL-1995 (first entry)  
XX XX  
XX Type I RIP gelonin analog Gel(C103).  
XX Type I ribosome-inactivating proteins; RIPs; gelonin;  
KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
KW graft-versus-host disease.  
XX Gelonium multiflorum.  
XX W09426910-A1.  
XX 24-NOV-1994.  
XX 12-MAY-1994; 94WO-US005348.  
XX 12-MAY-1993; 93US-00064691.  
XX (XOMA ) XOMA CORP.  
XX Better MD, Carroll SF, Studnicka GW;  
XX WPI; 1995-006804/01.  
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
XX are suitable for use as components of cytotoxic therapeutic agents.  
XX Example 3; Page 187-188; 221pp; English.  
XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
CC

CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 251 AA;

Query Match 99.0%; Score 1264; DB 2; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 1e-118; Mismatches 3; Indels 0; Gaps 0;  
 Matches 248; Conservative 0;  
 QY 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKADDDPGKAFVLVALSNDN 60  
 DB 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKADDDPGKCFVLVALSNDN 60  
 QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120  
 DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAISSLLVVIOMVSEARFTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAISSLLVVIOMVSEARFTFIENQIRNN 180  
 QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 DB 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 13  
 AAR63921  
 ID AAR63921 standard; protein; 251 AA.  
 XX  
 AC AAR63921;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 DE Type I RIP gelonin analog Gel (C10).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 XX Better MD, Carroll SF, Studnicka GW;  
 XX WPI; 1995-006804/01.  
 DR  
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 PS Example 3; Page 186; 221pp; English.  
 XX

CC AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 2e-118; Mismatches 3; Indels 0; Gaps 0;  
 Matches 248; Conservative 0;  
 QY 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKADDDPGKAFVLVALSNDN 60  
 DB 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKADDDPGKCFVLVALSNDN 60  
 QY 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120  
 DB 61 GOLAEIAIDVTSVYVVGQVNRNSYFFPKADPDAAYEGLFKNTIKTRLHFGGSYPSEGEK 120  
 QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAISSLLVVIOMVSEARFTFIENQIRNN 180  
 DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAISSLLVVIOMVSEARFTFIENQIRNN 180  
 QY 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 DB 181 FQQRIRPANNTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 QY 241 ALLKFVDKDPK 251  
 DB 241 ALLKFVDKDPK 251

RESULT 14  
 AAR63918  
 ID AAR63918 standard; protein; 251 AA.  
 XX  
 AC AAR63918;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JUL-1995 (first entry)  
 XX  
 DE Type I RIP gelonin analog Gel (C248).  
 XX  
 KW Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.  
 XX  
 OS Gelonium multiflorum.  
 XX  
 PN WO9426910-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 12-MAY-1994; 94WO-US005348.  
 XX  
 PR 12-MAY-1993; 93US-00064691.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 XX Better MD, Carroll SF, Studnicka GW;  
 XX WPI; 1995-006804/01.  
 DR  
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.  
 XX  
 PS Example 3; Page 183-184; 221pp; English.  
 PS

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 2e-118;  
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKAFVLVALSNDN 60  
 Db 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKCFVLVALSNDN 60  
 Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180  
 Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180  
 Qy 181 FQQRIRPANNTISLENKWGKLSFOIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 Db 181 FQQRIRPANNTISLENKWGKLSFOIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 Qy 241 ALLKFVDKDPK 251  
 Db 241 ALLKFVDKDPK 251

## RESULT 15

AAR63920  
 ID AAR63920 standard; protein; 251 AA.

XX AAR63920;

XX 25-MAR-2003 (revised)  
 XX 27-JUL-1995 (first entry)

XX Type I RIP gelonin analog Gel (C244).

XX Type I ribosome-inactivating proteins; RIPs; gelonin;  
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
 KW graft-versus-host disease.

XX Gelonium multiflorum.

XX WO9426910-A1.

XX 24-NOV-1994.

XX 12-MAY-1994; 94WO-US005348.

XX 12-MAY-1993; 93US-00064691.

XX (XOMA ) XOMA CORP.

XX Better MD, Carroll SF, Studnicka GW;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins - which  
 PT are suitable for use as components of cytotoxic therapeutic agents.

XX

PS Example 3; Page 185; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating  
 CC protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911.  
 CC RIPs are key components of cytotoxic therapeutic agents (CTAs), which  
 CC include gene fusion products and immunoconjugates. CTAs may be used to  
 CC selectively eliminate any cell type to which a RIP component is  
 CC targeted, by the specific binding capacity of the second component of  
 CC the agent. They can be used in the treatment of diseases where the  
 CC elimination of a particular cell type is desired, such as autoimmune  
 CC disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

SQ Sequence 251 AA;

Query Match 98.7%; Score 1261; DB 2; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 2e-118;  
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKAFVLVALSNDN 60  
 Db 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHSHGIPLLRKADDPGKCFVLVALSNDN 60  
 Qy 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 Db 61 GOLAEIAIDVTSVYVVGQVNRNSYFFKADPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
 Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180  
 Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARPTFIENQIRNN 180  
 Qy 181 FQQRIRPANNTISLENKWGKLSFOIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 Db 181 FQQRIRPANNTISLENKWGKLSFOIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
 Qy 241 ALLKFVDKDPK 251  
 Db 241 ALLKFVDKDPK 251

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 Job time : 137.614 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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(without alignments)  
704.723 Million cell updates/sec  
Title: US-10-717-243-101  
Perfect score: 1277  
Sequence: 1 GLDTSVSTKGTATYTYNPF.....AVDQVKPKIALLKFDKDPK 251  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	99.4	316	2	JT0753
2	353.5	27.7	245	2	JC4840
3	348	27.3	286	2	S25560
4	346	27.1	576	1	RLCSD
5	343	26.9	286	2	JC4235
6	337.5	26.4	564	1	RLCSAG
7	334.5	26.2	527	2	S32430
8	332.5	26.0	294	2	S28421
9	330	25.8	251	2	C39761
10	327	25.6	313	2	S17757
11	323	25.3	289	1	RLT2T
12	321	25.1	528	1	TZLSA
13	317	24.8	247	2	JU0393
14	317	24.8	289	2	JCS606
15	313.5	24.5	261	2	JE0401
16	312	24.4	247	2	JCS032
17	310.5	24.3	277	2	S22494
18	304.5	23.8	254	2	PD0018
19	299	23.4	528	2	S32431
20	299	23.4	562	2	S16022
21	292	22.9	286	1	RLPUGG
22	290.5	22.7	570	2	S62627
23	287.5	22.5	278	2	JN0108
24	274	21.5	250	2	S32431
25	215.5	16.9	278	2	A39817
26	210	16.4	272	2	JC4811
27	204	16.0	310	2	S42339
28	195	15.3	40	2	S17574
29	184.5	14.4	253	2	S28542

ALIGNMENTS

RESULT 1

JT0753  
rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum  
N:Alternate names: gelonin; type I ribosome-inactivating protein  
C:Species: Gelonium multiflorum  
C>Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: JT0753; S16489  
R:Nolan, P.A.; Garrison, D.A.; Better, M.  
Gene 134, 223-227, 1993  
A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein  
A:Reference number: JT0753; MUID:94085781; PMID:7916721  
A:Accession: JT0753  
A:Molecule type: mRNA  
A:Residues: 1-316 <NOI>  
R:Cross-references: UNIPROT:P33186; UNIPARC:UPI0000133948; GB:U12243; NID:9388633; PIDN:R1000000000; P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Sorie, M.; Lappi, D.  
Int. J. Pept. Protein Res. 33, 263-267, 1989  
A:Title: N-terminal sequence of some ribosome-inactivating proteins.  
A:Reference number: S16331; MUID:89326691; PMID:2753596  
A:Accession: S16489  
A:Molecule type: protein  
A:Residues: 47-89, 'K', 91-92, 'D' <MON>  
A:Cross-references: UNIPARC:UPI0000177F26  
C:Function:  
A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase  
F:1-46/Domain: signal sequence #status predicted <Sig>  
F:47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>  
F:53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 99.4%; Score 1269; DB 2; Length 316;

Best Local Similarity 99.2%; Pred. No. 5.7e-97;

Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	GLDTSVSTKGTATYTYNPNELRVKLPKGNHGIPLLRKADDPGKAFVLVSLNDN	60
DB	47	GLDTSVSTKGTATYTYNPNELRVKLPKGNHGIPLLRKADDPGKCFVLVSLNDN	106
QY	61	QQLAIAIDVTSVYVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGSGSYPSLEGK	120
DB	107	QQLAIAIDVTSVYVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGSGSYPSLEGK	166
QY	121	AYRETTDGIPLRIGIKLDENADIDNKPTEIASLLVWVOMSEARFTFIENQIRNN	180
DB	167	AYRETTDGIPLRIGIKLDENADIDNKPTEIASLLVWVOMSEARFTFIENQIRNN	226
QY	181	FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI	240
DB	227	FOQIRPANNTISLENKWKLSFOIRTSANGMFSEAELEERANGKYYVTAVDQVKPKI	286
QY	241	ALLKFDKDPK 251	

rRNA N-glycosidase  
rRNA N-glycosidase  
rRNA N-glycosidase  
rRNA N-glycosidase  
rRNA N-glycosidase  
rRNA N-glycosidase  
rRNA N-glycosidase  
rRNA N-glycosidase  
N conserved hypoch  
abin (clone 3.7)  
tritin - wheat  
rRNA N-glycosidase  
hypothetical prote  
30K ribosome inact  
protein synthesis

Db 287 ALLKFPVDKDPK 297  
|||||  
RESULT 2  
JC4840  
rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd  
C;Species: Trichosanthes anguina (snake gourd)  
C;Date: 15-Aug-1996 #sequence\_revision 24-Oct-1997 #text\_change 05-Dec-1997  
C;Accession: JC4840; J070701; J0677  
R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.  
Biomed. Sci. 3, 178-186, 1996  
A;Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from  
A;Reference number: JC4840  
A;Accession: JC4840  
A;Molecule type: protein  
A;Residues: 1-132, 'S', 134-245 <CHO1>  
A;Cross-references: UNIPARC:UPI0000177F1A  
A;Experimental source: seed  
A;Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table  
R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.  
submitted to JIPID, August 1995  
A;Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from  
A;Reference number: J0677  
A;Accession: J070701  
A;Molecule type: protein  
A;Residues: 1-50, 'L', 52-245 <CHO2>  
A;Cross-references: UNIPARC:UPI0000177F1B  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C;Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed  
F;4-242/Domain: rRNA N-glycosidase homology <RNG>  
F;51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;70,158,161/Active site: Tyr, Glu, Arg #status predicted  
F;155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
Query Match 27.7%; Score 353.5; DB 2; Length 245;  
Best Local Similarity 36.3%; Pred. No. 9.5e-22;  
Matches 91; Conservative 44; Mismatches 95; Indels 21; Gaps 7;  
QY 5 VSFSTKGATITVYVNFNLRLVKLKPEGNHSHGIPILLRKKADDPGKAPVLVALSNDNGOLA 64  
Db 2 VSFDLSTATKKSYSFTQURDALPTQGTGVIGIPLIPSTASG-SQRFPRFNLTYNDET 60  
QY 65 EIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLE---GEKA 121  
Db 61 TVAVDVTVVYVAVRADAVSYFFEDTPAEAFKLIAGTKTVKLPGSYNDKLSQVVGKQ- 119  
QY 122 YRETTDLGIEPLRIGIKLDENAI--YKPTETIASLLVQMVSEARPTFIENQIR 178  
Db 120 -RDMIELGIPAL-----SSAITNMVYDYQSTAAALVLQSTAEARVYIEQQVS 170  
QY 179 NNFQRIIPANNTISLENKWKLSFOITSG--ANGMFSEAVELERANGKYYV--TAVD 234  
Db 171 SHLSSNFPNQAVISLENKWKLSKQIQIANRTGHGQFENPVELYNPDGTRFSVYTSAG 230  
QY 235 QVKPKIALKLF 245  
Db 231 VVRGNKILLY 241  
RESULT 3  
S25560  
rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple  
C;Species: Momordica balsamina (balsam apple)  
C;Date: 25-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: S25560  
R;Ortigue, M.; Better, M.  
Nucleic Acids Res. 20, 4662, 1992  
A;Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homol  
A;Reference number: S25560; MUID:93027170; PMID:1408771  
A;Accession: S25560  
A;Status: preliminary  
A;Molecule type: mRNA

A;Residues: 1-286 <ORT>  
A;Cross-references: UNIPROT:P29339; UNIPARC:UPI0000133937; EMBL:Z12175; NID:g19525; PID:  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C;Keywords: glycosidase; hydrolase  
F;27-264/Domain: rRNA N-glycosidase homology <RNG>  
Query Match 27.3%; Score 348; DB 2; Length 286;  
Best Local Similarity 37.4%; Pred. No. 3.3e-21;  
Matches 91; Conservative 34; Mismatches 108; Indels 10; Gaps 5;  
QY 5 VSFSTKGATITVYVNFNLRLVKLKPEGNHSHGIPILLRKKADDPGKAPVLVALSNDNGOLA 64  
Db 25 VNFDSLSTATKTYTFIEDFRATLFPESHKVVDIPLIYSTISD-SRRFILLDLTSTAYETI 83  
QY 65 EIAIDVTSVYVGVQVRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLE-GEKAYR 123  
Db 84 SVAIDVTNVYVAVYTRDVSYPFKESPPEAYNILFKGRKITLPTVGTNYENLQTAHKIR 143  
QY 124 ETTDLGIEPLRIGIKLDENAI--YKPTETIASLLVQMVSEARPTFIENQIRNFFQ 183  
Db 144 ENIDLGLPALSSAI-----TTLFYNAQSAPSAALLVLIQTAAARFKYIERHVAKYVAT 198  
QY 184 RIRPANNTISLENKWKLSFOI-RTSGANGMFSEAVELERANGKYYVTVAVDQ--VKPKI 240  
Db 199 NFKPNLAIISLENQWSALSQKIFLAQNGGKFRNPVDLIKPTGERFQVTNVDSDVVGNI 258  
QY 241 ALL 243  
Db 259 KLL 261  
RESULT 4  
RLCSD  
ricin D precursor - castor bean  
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C;Species: Ricinus communis (castor bean)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903  
R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.  
Nucleic Acids Res. 13, 8019-8033, 1985  
A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.  
A;Reference number: A24041; MUID:86067214; PMID:2999712  
A;Accession: A24041  
A;Molecule type: DNA  
A;Residues: 1-576 <HAL>  
R;Tregear, J.W.; Roberts, L.M.  
Plant Mol. Biol. 18, 515-525, 1992  
A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene  
A;Reference number: S20513; MUID:92163016; PMID:1371405  
A;Accession: S20513  
A;Molecule type: DNA  
A;Residues: 1-576 <TRE>  
A;Cross-references: UNIPARC:UPI00001338E8; EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:  
R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.  
Eur. J. Biochem. 148, 265-270, 1985  
A;Title: Nucleotide sequence of cloned cDNA coding for preproricin.  
A;Reference number: A24614; MUID:85179479; PMID:3838723  
A;Accession: A24614  
A;Molecule type: mRNA  
A;Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>  
A;Cross-references: UNIPARC:UPI000011D47E; GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:  
R;Yoshitake, S.; Funatsu, G.; Funatsu, M.  
Agric. Biol. Chem. 42, 1267-1274, 1978  
A;Title: Isolation and sequences of peptic peptides, and the complete sequence of ile c  
A;Reference number: A03372  
A;Accession: A03372  
A;Molecule type: protein  
A;Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>  
A;Cross-references: UNIPARC:UPI0000174677  
A;Note: this paper cites the others in the series providing experimental details for th  
R;Araki, T.; Funatsu, G.  
PEBS Lett. 191, 121-124, 1985



1

J. Biol. Chem. 260, 15682-15686, 1985  
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
A;Reference number: A24261; MUID:86059449; PMID:2999130  
A;Accession: A24261  
A;Molecule type: mRNA  
A;Residues: 1-564 <ROB>  
A;Cross-references: UNIPROT:P06750; UNIPARC:UPI00001256B9; GB:M12089; NID:g169700; PIDN:  
R;Araki, T.; Yoshioka, Y.; Funatsu, G.  
Biochim. Biophys. Acta 872, 277-285, 1986  
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti  
A;Reference number: A24210  
A;Accession: A24210  
A;Molecule type: protein  
A;Residues: 303-325, F, 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-  
A;Cross-references: UNIPARC:UPI0000174679  
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-290/Product: agglutinin chain A #status predicted <ACH>  
F;35-281/Domain: rRNA N-glycosidase homology <RNG>  
F;303-564/Product: agglutinin chain B #status experimental <BCH>  
F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats  
F;34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;104,147,231,232/Binding site: substrate (Tyr, Glu, Asn) #status predicted  
F;202,203/Active site: Glu, Arg #status predicted  
F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted  
F;324,337,348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted  
F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
Query Match 26.4%; Score 337.5; DB 1; Length 564;  
Best Local Similarity 36.3%; Pred. No. 6.1e-20;  
Matches 91; Conservative 42; Mismatches 105; Indels 13; Gaps 7;  
QY 5 VPSSTKGATITVYVNFLELRLVKLPKPGN-SHGIPILRKKADDP-GKAFVLVSLNDNGQ 62  
DB 33 INETTDADVESYTNFIRAVRSHLTGADVRRHIEPVLPRVGLPIQSRFILVELSHAE 92  
QY 63 LABIAIDVTSVVVGVQVNRYSFFKADPD-----AAYEGLFKNTIKT-RLHFGGSYPSL 116  
DB 93 SVTLALDVINAVVGCAGNSAYFFH--PDNQEDAEATHLFDVQNSFTFAFGGNYDL 150  
QY 117 EGEKAVRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQMVSEARFTPIENQ 176  
DB 151 EQLGGLRENIELGTGLEDAISALYYSTGCTQIPTLARSFMVCIQMISEARFQYIEGE 210  
QY 177 IRN-NFOQIRPANNTISLENKWKLSQIRTSANGMFSEAVELERANGKYYVAVD 234  
DB 211 MTRIRNRRSAPDPSPVITLNSWGLRSLTAIQESN-QGAPASPIQLQRNGSKFNVDVS 269  
QY 235 QVKPKIALLK 245  
DB 270 ILIPITALWY 280  
RESULT 7  
abrin-b precursor - Indian licorice (fragment)  
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C;Species: Abrus precatorius (Indian licorice)  
C;Date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: S32430; JCI1399  
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
J. Mol. Biol. 229, 263-267, 1993  
A;Title: Primary structure of three distinct isoabrin determined by cDNA sequencing. Co  
A;Reference number: S32429; MUID:93122798; PMID:8421313  
A;Accession: S32430  
A;Molecule type: mRNA  
A;Residues: 1-527 <HUN>  
A;Cross-references: UNIPROT:Q06077; UNIPARC:UPI0000125160; GB:M98345; NID:g166296; PIDN:  
R;Kimura, M.; Sumizawa, T.; Funatsu, G.  
Biosci. Biotechnol. Biochem. 57, 166-169, 1993

A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxi  
A;Reference number: JCI1398; MUID:93169023; PMID:7763422  
A;Accession: JCI1399  
A;Molecule type: protein  
A;Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430  
A;Cross-references: UNIPARC:UPI00001772PA  
A;Experimental source: seed  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; r  
F;1-250/Product: abrin-b chain A #status predicted <ACH>  
F;7-245/Domain: rRNA N-glycosidase homology <RNG>  
F;260-527/Product: abrin-b chain B #status experimental <BCH>  
F;282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
F;74,113,194,195/Binding site: substrate (Tyr, Glu, Asn) #status predicted  
F;110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;163,166/Active site: Glu, Arg #status predicted  
F;246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted  
F;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
Query Match 26.2%; Score 334.5; DB 2; Length 527;  
Best Local Similarity 37.7%; Pred. No. 9.9e-20;  
Matches 97; Conservative 34; Mismatches 103; Indels 23; Gaps 9;  
QY 5 VPSSTKGATITVYVNFLELRLVKLPKPGN-SHGIPILRKKADDP-----GKAFVLVSLND 59  
DB 5 IKFTTTEGATSQYKQFIALRQL-TGGILHGIPLV----PDPTLQERNYISVELSNS 59  
QY 60 NQLAEIAIDVTSVVVGVQVNRYSFFKADPDAAVEGLFKNTIKTRLHFGGSPSLEG- 118  
DB 60 DTESIETAGIDVSNVAVVYRAGNRSYFURDAPTSRVLFTQTSYLRFGNSYIDLRL 119  
QY 119 EKAYRETTDLGIEPLRIGIKKLDENADINYPKPTIASLLVVIQMVSEARFTPIENQ-- 176  
DB 120 ARQTRQIPLGLQALRHAIISFLQSGTDQ----EIARTLIVIIQASEARVRFISYRVG 175  
QY 177 --IRNFQOIRPANNTISLENKWKLSQIRTSANGMFSEAVELERANGKYYVAV- 233  
DB 176 VSIRTN--TAFQPDAMISLENNDLNSGGVQQS--VDPTFPNAVTLRSVNNQFVDSLT 232  
QY 234 DVQPKIALLK 250  
DB 233 HOSVAVLALMLFVCNPP 249  
RESULT 8  
S28421  
rRNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed  
N;Alternate names: antiviral protein alpha-PAP  
C;Species: Phytolacca americana (Virginian pokeweed)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
A;Accession: S28421  
R;Katsoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koiwai, A.  
Plant Mol. Biol. 20, 879-886, 1992  
A;Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein  
A;Reference number: S28421; MUID:93099240; PMID:1281438  
A;Accession: S28421  
A;Molecule type: DNA  
A;Residues: 1-294 <KAT>  
A;Cross-references: UNIPROT:Q03464; UNIPARC:UPI0000133946; EMBL:D10600; NID:g218010; PFI  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C;Keywords: glycosidase; hydrolase  
F;30-278/Domain: rRNA N-glycosidase homology <RNG>  
Query Match 26.0%; Score 332.5; DB 2; Length 294;  
Best Local Similarity 32.2%; Pred. No. 6.5e-20;  
Matches 85; Conservative 50; Mismatches 102; Indels 27; Gaps 8;  
QY 2 LDTVSFSTKGATITVYVNFLELRLVKLK-PEGNSHGIPILRKKADDPGKAFVLVSLNDN 60  
DB 25 INTITFDVGNATINKYATPMKSIHQAKQDPTLKCYGIPMLPNTNLTTP--KYLAVTLQDSS 82





**RESULT 13**

JU0393  
karasurin - Mongolian snake-gourd  
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: JU0393; PS0163  
R;Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogiwara, Y.  
Chem. Pharm. Bull. 39, 1244-1249, 1991  
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin.  
A;Reference number: JU0393; MUID:92005921; PMID:1914000  
A;Accession: JU0393  
A;Molecule type: protein  
A;Residues: 1-247 <TOY>  
A;Cross-references: UNIPROT:P24478; UNIPARC:UPI000015667C  
A;Note: a sequence which lacks Ala-247 is also shown in this publication  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C;Keywords: abortifacient  
F;4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 24.8%; Score 317; DB 2; Length 247;  
Best Local Similarity 38.2%; Pred. No. 9.7e-19;  
Matches 94; Conservative 33; Mismatches 105; Indels 14; Gaps 8;

Qy 5 VSFSTKATYTIVYNFLNELRVKLKEGNSHGICPIILRLKKADDPG-KAFVLVALSNDNGQL 63  
||| ||| :  
Db 2 VSFRLSGATSSYGVSFINLRALPYERKLYDIPLLRSTL--PGSQRYALIHITNYADET 59  
||| ||| :  
Qy 64 AEIADVTSVVVGVQVNRNRSYFFPKDA-PDAAYEGLFKNT-IKTRLHFGGSYPSE-GEK 120  
: ||| :  
Db 60 ISVAIDTVNVVMGYRADGTSYFFNEASATEAAKYVFDKAKRKVTLPYSGNVERLOIAAG 119  
: ||| :  
Qy 121 AYRETTDLGIPLRIGIKKLDENAIKNYKPTBIASLLVVIQMVSRAARTFTFIENQRNN 180  
||| ||| :  
Db 120 KIRENIPLGLPALDSAI-----TTLFYNNANSAALMVLIQISTSEAARYKFIEQQIGKR 174  
||| ||| :  
Qy 181 FQQRIRPANNWISLENKWKLSFQTR-TSGANGMSEAVELEBRANGKYYVTAVDQ--VK 237  
: : ||| :  
Db 175 VDKTFPLSLAIISLENSWSALSQIQIASTNNGQPETPVVLINAOQRVTTITNVDAGVVT 234  
||| ||| :  
Qy 238 PKIALL 243  
||| |||  
Db 235 SNIALL 240  
||| |||

**RESULT 14**

JC5606  
karasurin C - Trichosanthes kirilowii var. japonica  
N;Contains: karasurin A  
C;Species: Trichosanthes kirilowii var. japonica  
C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: JC5606; JC5033  
R;Mizukami, H.; Iida, K.; Kondo, T.; Ogiwara, Y.  
Biol. Pharm. Bull. 20, 711-713, 1997  
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protease  
A;Reference number: JC5606; MUID:97356562; PMID:9212998  
A;Accession: JC5606  
A;Molecule type: DNA  
A;Residues: 1-289 <MIZ>  
A;Cross-references: UNIPROT:P24478; UNIPARC:UPI000013394C; DDBJ:AB0000666; NID:92329830;  
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.  
Biol. Pharm. Bull. 19, 1485-1489, 1996  
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and k  
A;Reference number: JC5032; MUID:97108848; PMID:8951169  
A;Accession: JC5033  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 22-270 <KON>  
A;Cross-references: UNIPARC:UPI0000177F1D  
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
F;22-270/Product: karasurin C #status predicted <MAC>  
F;24-270/Product: karasurin A #status predicted <MAA>

Search completed: February 10, 2006, 10:14:06  
Job time : 35.2694 secs

Qy	5	V	S	F	S	T	K	G	A	T	I	T	T	V	N	F	L	N	E	L	R	V	K	L	K	P	E	G	N	S	H	G	I	P	L	L	R	K	A	D	D	G	-	K	A	F	V	L	V	A	L	S	N	D	N	C	Q	L	63
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
Db	25	V	F	R	L	G	A	T	S	S	G	V	F	I	N	R	K	A	L	P	Y	E	R	K	L	D	I	P	L	L	R	T	L	--	P	G	S	O	R	V	A	L	I	H	T	N	A	D	E	T	82								

**Qy**      64 A E I A D V T S V V V G Y Q V N R S Y F P K D A - P D A A Y E G L F K N T - I K T R L H F G G S Y P S L E - C E K 120  
              | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
**Dd**      83 I S V A I D V T N V V M G Y R A G D T S Y F F N E A S A T E A A K Y V F D K A R K V T L P T S G N Y E R L Q T A A G 142

Qy	121	AVRETTDLGIEPLRIGIKKLDENAI	DNYKPTFIASSLLVVIQMVSEARFT	FTEINQIRNN	180
Db	143	KIRENIPLGLPALDSAI	-----TTLFYNNANSAASALMVL	IOSTSEAAKYKFTEOOIGKR	197

Qy	181	FOQIRPANNTISLENKWGLSFQIR-TSGANGMFSEAVELERANGKKYVTVADQ--VK	237
Db	198	VPKTELPALATISLENSWSAIKFOIOTASTNNCOFETPVLNAONRVTITNVDAGVYT	257

Qy 238 PKIALL 243  
Db 258 SNIAJ. 263

RESULT 15

JE0401

antiviral protein - Virginian pokeweed

C/Species: *Phytolacca americana* (Virginian pokeweed)

C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004

C/Accession: JE0401

R/Kung, S.S.; Kimura, M.; Funatsu, G.

Agric. Biol. Chem. 54, 3301-3318, 1990

A/Title: The complete amino acid sequence of antiviral protein from the seeds of pokeweed

A/Reference number: JE0401; MUID: 91242096; PMID: 1368643

A/Accession: JE0401

A/Molecule type: protein

A/Residues: 1-261 <KUN>

A/Cross-references: UNIPROT:P23339; UNIPARC:UPI0000013394B

A/Experimental source: seed

C/Comment: This protein prevents the replication of a number of plant viruses, and inhibits the replication of tobacco etch virus.

C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C/Keywords: disulfide bond; glycoprotein

F/6-254/Domain: rRNA N-glycosidase homology <RNG>

F/10, 44, 255/Binding site: carbohydrate (Asn) (covalent) #status experimental

F/34-258, 84-105/disulfide bonds: #status experimental

Query Match 24.5%; Score 313.5; DB 2; Length 261;  
Best Local Similarity 32.4%; Pred. No. 2e-18;  
Matches 85; Conservative 49; Mismatches 105; Indels 23;  
Gaps 9;

Qy	2	LDTVSFSTKGATVITYVNFNLNLRVKLK-PEGNSHGIPILLRKKADDPGKAFVLVALSNDN	60
Dh	1	ITNITFAGNATNKNYATETMESIPNEAPDPSICVGIIMLDEL--TNSITKVLKTKIGCAS	58

QY 61 GOLAEIAIDVTSVVVG---YQVRNRSYFFKADPAAEGLFKNT-----IKTRLH 108

[illegible][illegible]

Qy 226 KKYVTVAVDQVKPIALLKFVD 247  
| : | : | : | : | : | :  
234 TKTATG EIMTQYKIDQYI NTCY 255

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:00:34 ; Search time 212.1 Seconds  
(without alignments)  
834.927 Million cell updates/sec

Title: US-10-717-243-101  
Perfect score: 1277  
Sequence: 1 GLDTSSTKATYTYVNF.....AVDQVKPALKKFDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1269	99.4	316	1 RIPG_GELMU	P33186 gelonium mu
2	1235.5	96.8	258	2 Q9S9E4_GELMU	Q9S9E4 gelonium mu
3	398.5	31.2	581	2 Q94BW5_CINCA	Q94BW5 cinnamomum
4	397.5	31.1	580	2 Q94BW3_CINCA	Q94BW3 cinnamomum
5	396.5	31.0	549	2 Q9FV22_CINCA	Q9FV22 cinnamomum
6	391	30.6	299	2 Q8GZ99_9ROSI	Q8GZ99 euphorbia s
7	390.5	30.6	580	2 Q94BW4_CINCA	Q94BW4 cinnamomum
8	365.5	28.6	563	2 Q8GT32_SAMNI	Q8GT32 sambucus ni
9	359.5	28.2	297	2 Q8GZP0_9ROSI	Q8GZP0 euphorbia s
10	356	27.9	563	2 NIGB_SAMNI	P33183 sambucus ni
11	356	27.9	563	2 Q94S52_SAMNI	Q94S52 sambucus ni
12	352.5	27.6	563	2 Q04367_SAMNI	Q04367 sambucus ni
13	348	27.3	264	2 Q684J5_MOMCH	Q684J5 momordica b
14	348	27.3	286	1 RIP2_MOMCH	P24817 momordica c
15	348	27.3	286	1 RIP3_MOMCH	P24817 momordica c
16	348	27.3	286	2 Q5PZ05_MOMCH	Q5PZ05 momordica c
17	347	27.2	541	2 Q41174_RICCO	Q41174 ricinus com
18	346	27.1	576	1 RIC1_RICCO	P02879 ricinus com
19	343.5	26.9	265	1 RIP2_PHYDI	P34967 phytolacca
20	341.5	26.7	294	1 RIP1_TRIAN	P56626 trichosanthe
21	341.5	26.7	564	2 Q9AVR2_9DIPS	Q9AVR2 sambucus eb
22	337.5	26.4	564	1 AGSL_RICCO	P06750 ricinus com
23	337	26.4	282	1 RIP2_BRYDI	P98184 bryonia dio
24	334.5	26.2	527	1 ABRP_ABRPR	Q05077 abrus preca
25	332.5	26.0	294	1 RIPA_PHYAM	Q03464 phytolacca
26	330.5	25.9	293	2 Q8YVU0_9ROSI	Q8YVU0 jatrophia cu
27	330	25.8	252	2 Q38760_ABRPR	Q38760 abrus preca
28	329.5	25.8	294	2 Q8H1W1_PHYAM	Q8H1W1 phytolacca
29	328.5	25.7	275	2 Q84LJ1_GYNPE	Q84LJ1 gynostemma
30	327.5	25.6	277	2 Q84JRI_GYNPE	Q84JRI gynostemma
31	327	25.6	313	1 RIP1_PHYAM	P10297 phytolacca

32	327	25.6	313	2 Q6PWU4_PHYAM	Q6PWU4 phytolacca
33	327	25.6	313	2 Q53YN2_PHYAM	Q53YN2 phytolacca
34	326.5	25.6	277	2 Q8GV09_GYNPE	Q8GV09 gynostemma
35	326	25.5	289	2 Q41216_TRIKI	Q41216 trichosanthe
36	325.5	25.5	275	2 Q8H1Y4_GYNPE	Q8H1Y4 gynostemma
37	325.5	25.5	293	2 Q8S452_9ROSI	Q8S452 jatrophia cu
38	325.5	25.5	298	2 Q5F013_GYNPE	Q5F013 gynostemma
39	325	25.5	567	2 Q6H267_VISAL	Q6H267 viscum albu
40	323.5	25.3	277	2 Q8GV11_GYNPE	Q8GV11 gynostemma
41	323	25.3	289	1 RIPT_TRIKI	P09989 trichosanthe
42	323	25.3	289	2 Q94KE4_TRIKI	Q94KE4 trichosanthe
43	322	25.2	289	2 Q84SV8_TRIKI	Q84SV8 trichosanthe
44	321.5	25.2	565	2 Q04071_SAMNI	Q04071 sambucus ni
45	321	25.1	251	2 Q7DM12_ABRPR	Q7DM12 abrus preca

## ALIGNMENTS

RESULT 1					
ID	RIPG_GELMU	STANDARD;	PRT;	316 AA.	
AC	P33186;				
DT	01-OCT-1993	(Rel. 27, Created)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	10-MAY-2005	(Rel. 47, Last annotation update)			
DB	Ribosome-inactivating protein gelonin precursor	(EC 3.2.2.22) (rRNA N-glycosidase).			
GN	Name=GEL;				
OS	Gelonium multiflorum (Euphorbiaceae himalayana).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
OC	rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;				
OC	Geloniae; Gelonium.				
OX	NCBI_TaxID=3979;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=94085781; PubMed=7916721; DOI=10.1016/0378-1119(93)90097-M;				
RA	Nolan P.A., Garrison D.A., Better M.;				
RT	"Cloning and expression of a gene encoding gelonin, a ribosome-				
RT	inactivating protein from Gelonium multiflorum.";				
RL	Gene 134:223-227(1993).				
RN	[2]				
RP	PROTEIN SEQUENCE OF 47-93.				
RC	TISSUE=Seed;				
RX	MEDLINE=89326691; PubMed=2753596;				
RA	Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe P., Soria M.,				
RA	Lappi D.;				
RT	"N-terminal sequence of some ribosome-inactivating proteins.";				
RL	Int. J. Pept. Protein Res. 33:263-267(1989).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RX	MEDLINE=95333189; PubMed=7608981;				
RA	Hosur M.V., Nair B., Sathyamurthy P., Misquith S., Suroolia A.,				
RA	Kannan K.K.;				
RT	"X-ray structure of gelonin at 1.8-A resolution.";				
RL	J. Mol. Biol. 250:368-380(1995).				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one				
CC	specific adenosine on the 28S rRNA.				
CC	-1- SUBUNIT: Homodimer.				
CC	-1- SIMILARITY: Belongs to the ribosome-inactivating protein family.				
CC	Type 1 RIP subfamily.				
CC	-----				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use as long as its content is in no way modified and this statement is not				
CC	removed.				
CC	-----				
DR	EMBL; L12243; AAA16312.1; -; mRNA.				
DR	PIR; J07533; J07533.				
DR	HSSP; P09989; LMRJ.				
DR	InterPro; IPR001574; RIP.				

DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;  
 KW Protein synthesis inhibitor; Signal; Toxin.  
 FT SIGNAL 1 26 Potential.  
 FT PROPEP 27 46  
 FT CHAIN 47 297  
 FT PROPEP 298 316 Ribosome-inactivating protein gelonin.  
 FT ACT SITE 212 232 Removed in mature form.  
 FT CARBOHYD 235 235 N-linked (GlcNAc...).  
 FT DISULFID 90 96  
 FT CONFLICT 90 90 C -> K (in Ref. 2).  
 FT CONFLICT 93 93 P -> D (in Ref. 2).  
 SQ SEQUENCE 316 AA; 35419 MW; 1252F3E710901B85 CRC64;

Query Match 99.4%; Score 1269; DB 1; Length 316;  
 Best Local Similarity 99.2%; Pred. No. 1.9e-97;  
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKADDPGKAFVLVALSNDN 60  
 |||||  
 DB 47 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKADDPGKCFVLVALSNDN 106  
 |||||

QY 61 GLAEIAIDVTSVYVGVQVNRNRSFFPKDAPDAAYEGLFKNTIKRLHFGGSPSLEGEK 120  
 |||||  
 DB 107 GLAEIAIDVTSVYVGVQVNRNRSFFPKDAPDAAYEGLFKNTIKRLHFGGSPSLEGEK 166  
 |||||

QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 180  
 |||||  
 DB 167 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTFIENQIRNN 226  
 |||||

QY 181 FQOIRPNANTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240  
 |||||  
 DB 227 FQOIRPNANTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 286  
 |||||

QY 241 ALLKFKVDKPK 251  
 |||||  
 DB 287 ALLKFKVDKPK 297  
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RESULT 2  
 Q9S9E4\_GELMU PRELIMINARY; PRT; 258 AA.  
 ID Q9S9E4; GELMU PRELIMINARY; PRT; 258 AA.  
 AC Q9S9E4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).  
 OS Gelonium multiflorum (Euphorbiaceae Himalaya).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;  
 OC Geloniae; Gelonium.  
 OC NCBI\_TaxID=3979;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=96006751; PubMed=7553224;  
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,  
 RA Toman P.D., Cheung L.;  
 FT "Amino acid sequence analysis, gene construction, cloning, and  
 RT expression of gelonin, a toxin derived from Gelonium multiflorum.";  
 RL J. Interferon Cytokine Res. 15:547-555(1995).  
 DR HSSP; P09989; 1MRJ.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
 DR GO; GO:0005952; P:defense response; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.  
 SQ SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 96.8%; Score 1235.5; DB 2; Length 258;  
 Best Local Similarity 95.4%; Pred. No. 9.3e-95;  
 Matches 247; Conservative 1; Mismatches 2; Indels 9; Gaps 2;

QY 1 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKADDPGKAFVLVALSNDN 60  
 |||||  
 DB 1 GLDTSVSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLR-KGDDPGKCFVLVALSNDN 59  
 |||||

QY 61 GLAEIAIDVTSVYVGVQVNRNRSFFPKDAPDAAYEGLFKNTI-----KTRLHFGGS 112  
 |||||  
 DB 60 GLAEIAIDVTSVYVGVQVNRNRSFFPKDAPDAAYEGLFKNTIKRPLLFQGTIKRLHFGGS 119  
 |||||

QY 113 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTF 172  
 |||||  
 DB 120 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQVSEAAARFTF 179  
 |||||

QY 173 IENQIRNNFQOIRPNANTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTA 232  
 |||||  
 DB 180 IENQIRNNFQOIRPNANTISLENKWKGLSFQIRTSANGMFSEAVELERANGKYYVTA 239  
 |||||

QY 233 VDQVKPKIALKFKVDKPK 251  
 |||||  
 DB 240 VDQVKPKIALKFKVDKPK 258  
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RESULT 3  
 Q94BW5\_CINCA PRELIMINARY; PRT; 581 AA.  
 ID Q94BW5; CINCA PRELIMINARY; PRT; 581 AA.  
 AC Q94BW5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor.  
 OS Cinnamomum camphora (Camphor tree).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;  
 OC Cinnamomum.  
 OC NCBI\_TaxID=13429;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;  
 RA Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;  
 RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated  
 RT from the seeds of camphor tree and their expression patterns.";  
 RL Gene 284:215-223(2002).  
 DR EMBL; AY039801; AAK82458.1; -; Genomic\_DNA.  
 DR HSSP; P02879; 2AAI.  
 DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 2.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SMO0458; RICIN; 2.  
 DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 KW SIGNAL.  
 FT SIGNAL 1 32 Potential.  
 FT CHAIN 33 581 type 2 ribosome-inactivating protein cinnamomin I.  
 SQ SEQUENCE 581 AA; 64215 MW; 6E8F5FB8FBA3D196 CRC64;

Query Match 31.2%; Score 398.5; DB 2; Length 581;  
 Best Local Similarity 39.7%; Pred. No. 1.8e-24;  
 Matches 100; Conservative 46; Mismatches 93; Indels 13; Gaps 8;

QY 4 TVSFSTKGATYITYVNFNLRLVRLKPEGNHSHGIPLLRKADDPGKAFVLVALSNDN 59  
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 DB 35 TVTFTTKNATKTSYTFQIFALRAQLASGEHPHGVNMRSTVPDSKRFILVELSNWAAD 94  
 |||||





[illegible]











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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 10, 2006, 10:37:59 ; Search time 163.937 Seconds  
(without alignments)  
639.727 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTRVSTKGTATVTVNF.....AVDQVKPAILLKFDVKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	100.0	251	4	US-10-127-890-101
2	1277	100.0	251	5	US-10-717-243-101
3	1273	99.7	251	4	US-10-127-890-99
4	1273	99.7	251	5	US-10-127-890-100
5	1273	99.7	251	5	US-10-717-243-99
6	1273	99.7	251	5	US-10-717-243-100
7	1269	99.4	251	3	US-09-765-527-247
8	1269	99.4	251	4	US-10-127-890-2
9	1269	99.4	251	4	US-10-127-890-110
10	1269	99.4	251	5	US-10-717-243-2
11	1269	99.4	251	5	US-10-717-243-110
12	1269	99.4	316	4	US-10-074-596-1
13	1269	99.4	498	5	US-10-964-195-13
14	1269	99.4	507	4	US-10-074-596-11
15	1266	99.1	293	3	US-09-765-527-259
16	1266	99.1	309	3	US-09-765-527-253
17	1266	99.1	332	3	US-09-765-527-251
18	1265	99.1	751	6	US-11-084-080-26
19	1264	99.0	251	4	US-10-127-890-108
20	1264	99.0	251	5	US-10-717-243-108
21	1261	98.7	251	4	US-10-127-890-103
22	1261	98.7	251	4	US-10-127-890-104
23	1261	98.7	251	4	US-10-127-890-105
24	1261	98.7	251	4	US-10-127-890-106
25	1261	98.7	251	4	US-10-127-890-109
26	1261	98.7	251	5	US-10-717-243-103
27	1261	98.7	251	5	US-10-717-243-104

28 1261 98.7 251 5 US-10-717-243-105 Sequence 105, App  
29 1261 98.7 251 5 US-10-717-243-106 Sequence 106, App  
30 1261 98.7 251 5 US-10-717-243-109 Sequence 109, App  
31 1260 98.7 251 4 US-10-127-890-102 Sequence 102, App  
32 1260 98.7 251 4 US-10-127-890-107 Sequence 107, App  
33 1260 98.7 251 4 US-10-127-890-111 Sequence 111, App  
34 1260 98.7 251 5 US-10-717-243-102 Sequence 102, App  
35 1260 98.7 251 5 US-10-717-243-107 Sequence 107, App  
36 1260 98.7 251 5 US-10-717-243-111 Sequence 111, App  
37 1212.5 94.9 513 5 US-10-926-731A-12 Sequence 12, Appl  
38 1201 94.0 506 5 US-10-964-195-11 Sequence 11, Appl  
39 348 27.3 263 4 US-10-127-890-4 Sequence 4, Appl  
40 348 27.3 263 5 US-10-717-243-4 Sequence 4, Appl  
41 346 27.1 267 4 US-10-282-935-1 Sequence 1, Appl  
42 346 27.1 267 4 US-10-127-890-1 Sequence 1, Appl  
43 346 27.1 267 4 US-10-440-796-1 Sequence 1, Appl  
44 346 27.1 267 5 US-10-717-243-1 Sequence 1, Appl  
45 346 27.1 576 4 US-10-083-336A-1 Sequence 1, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-127-890-101

; Sequence 101, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; APPLICATION NUMBER: PC7/US94/05348

; FILING DATE: 12-MAY-1994

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 200-70.P4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155

; TELEX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 101:

; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:  
US-10-127-890-101

Query Match 100.0%; Score 1277; DB 4; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.2e-115; Mismatches 0; Indels 0; Gaps 0;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60  
DB 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYSLSGEK 120  
DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYSLSGEK 120

QY 121 AYRETTDLGIEPLRIGIKGLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKGLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQQRIRPANNTISLENKKGKLSFQIRTSANGMPSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FQQRIRPANNTISLENKKGKLSFQIRTSANGMPSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

## RESULT 2

US-10-717-243-101  
; Sequence 101, Application US/10717243  
; Publication No. US20050054835A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/717,243  
; FILING DATE: 18-Nov-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/839,765  
; FILING DATE: 15-APR-1997  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:

;  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:  
US-10-717-243-101

Query Match 100.0%; Score 1277; DB 5; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.2e-115; Mismatches 0; Indels 0; Gaps 0;  
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60  
DB 1 GLDTVSFSTKGATITTYVNFNLRLVRLKPEGNHSHGIPLLRKKADDPGKAFVLVALSNDN 60

QY 61 GQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYSLSGEK 120  
DB 61 GQLAEIAIDVTSVYVVGQVNRNSYFFPKDAPDAAYEGLFKNTIKTRLHFGSGYSLSGEK 120

QY 121 AYRETTDLGIEPLRIGIKGLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKGLDENADINYPKTEIASLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQQRIRPANNTISLENKKGKLSFQIRTSANGMPSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FQQRIRPANNTISLENKKGKLSFQIRTSANGMPSEAVELERANGKYYVTVAVDQVKPKI 240

QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 3  
US-10-127-890-99  
; Sequence 99, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127,890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994

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;
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9155
;
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-127-890-99

Query Match          99.7%; Score 1273; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATITVYVFNELRVKLPKGNHSHGIPLLKAKDDPGKAPVLVSLNDN 60
DB 1 GLDTSVSTKGATITVYVFNELRVKLPKGNHSHGIPLLKAKDDPGKAPVLVSLNDN 60

QY 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
DB 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTKTEIASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTKTEIASSLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDKP 251
DB 241 ALLKFVDKDKP 251

RESULT 4
US-10-127-890-100
; Sequence 100, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
;
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-127-890-100

Query Match          99.7%; Score 1273; DB 4; Length 251;
Best Local Similarity 99.6%; Pred. No. 3e-115;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLDTSVSTKGATITVYVFNELRVKLPKGNHSHGIPLLKAKDDPGKAPVLVSLNDN 60
DB 1 GLDTSVSTKGATITVYVFNELRVKLPKGNHSHGIPLLKAKDDPGKAPVLVSLNDN 60

QY 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120
DB 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGSGYPSLGEK 120

QY 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTKTEIASSLLVVIQMVSEAAARFTFIENQIRNN 180
DB 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTKTEIASSLLVVIQMVSEAAARFTFIENQIRNN 180

QY 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
DB 181 FQOIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240

QY 241 ALLKFVDKDKP 251
DB 241 ALLKFVDKDKP 251

RESULT 5
US-10-717-243-99
; Sequence 99, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
```

;  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/717,243  
; FILING DATE: 18-Nov-2003  
; CLASSIFICATION: 530  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/839,765  
; FILING DATE: 15-APR-1997  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
;  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:  
US-10-717-243-99

Query Match 99.7%; Score 1273; DB 5; Length 251;  
Best Local Similarity 99.6%; Pred. No. 3e-115;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GLDVSFSTKGATITVYVNFNLNRVCLKPGENSHGIPLLRKKADDPGKAFVLVSLNDN 60  
DB 1 GLDVSFSTKGATITVYVNFNLNRVCLKPGENSHGIPLLRKKADDPGKAFVLVSLNDN 60  
  
QY 61 GOLAEIAIDVTSVYVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 61 GOLAEIAIDVTSVYVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
  
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAARFTFIENQIRNN 180  
  
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240  
  
QY 241 ALLKFVDKDPK 251  
DB 241 ALLKFVDKDPK 251

RESULT 6  
US-10-717-243-100  
; Sequence 100, Application US/10717243  
; Publication No. US20050054835A1  
; GENERAL INFORMATION:

;  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen P.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/717,243  
; FILING DATE: 18-Nov-2003  
; CLASSIFICATION: 530  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/839,765  
; FILING DATE: 15-APR-1997  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
;  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-10-717-243-100

Query Match 99.7%; Score 1273; DB 5; Length 251;  
Best Local Similarity 99.6%; Pred. No. 3e-115;  
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GLDVSFSTKGATITVYVNFNLNRVCLKPGENSHGIPLLRKKADDPGKAFVLVSLNDN 60  
DB 1 GLDVSFSTKGATITVYVNFNLNRVCLKPGENSHGIPLLRKKADDPGKAFVLVSLNDN 60  
  
QY 61 GOLAEIAIDVTSVYVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
DB 61 GOLAEIAIDVTSVYVGVQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120  
  
QY 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAARFTFIENQIRNN 180  
DB 121 AYRETTDLGIEPLRIGIKKLDENADINYPKTEIASLLVVIQWVSEAAARFTFIENQIRNN 180  
  
QY 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240  
DB 181 FQOIRPANNTISLENKWKLSFQIRTSANGMFMSEAVELERANGKYYVTVAVDQVKPKI 240  
  
QY 241 ALLKFVDKDPK 251

Db 241 ALLKFPVDKDPK 251

## RESULT 7

US-09-765-527-247  
; Sequence 247, Application US/09765527  
; Patent No. US2002006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 247:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:  
US-09-765-527-247

Query Match 99.4%; Score 1269; DB 3; Length 251;  
Best Local Similarity 99.2%; Pred. No. 7.2e-115;  
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHGIPLLRKADDPGKAPVLVSLNDN 60  
Db 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHGIPLLRKADDPGKAPVLVSLNDN 60  
Qy 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Db 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180  
Qy 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 240  
Db 181 FQQRIRPANNITISLENKWKLSFQIRTSANGMFSEAVELERANGKYYTAVDQVKPKI 240  
Qy 241 ALLKFPVDKDPK 251  
Db 241 ALLKFPVDKDPK 251

## RESULT 8

US-10-127-890-2  
; Sequence 2, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen P.  
; Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127,890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-127-890-2

Query Match 99.4%; Score 1269; DB 4; Length 251;  
Best Local Similarity 99.2%; Pred. No. 7.2e-115;  
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHGIPLLRKADDPGKAPVLVSLNDN 60  
Db 1 GLDTSVSTKGATVITYVNFNLRLVKLPKGNHGIPLLRKADDPGKAPVLVSLNDN 60  
Qy 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Db 61 GOLAEIAIDVTSVVVGQVNRNSYFFKADPAAYEGLFKNTIKTRLHFGGSYPSLSEK 120  
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180  
Db 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQWVSEAAARFTFIENQIRNN 180





Qy 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db 227 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 286  
Qy 241 ALLKFVDKDPK 251  
Db 287 ALLKFVDKDPK 297

RESULT 13  
US-10-964-195-13  
; Sequence 13, Application US/10964195  
; Publication No. US20050163774A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosenblum et al.  
; TITLE OF INVENTION: Immunotoxins Directed Against c-erbB-2 (HER-2/Neu)  
; FILE REFERENCE: D5425CIP2  
; CURRENT APPLICATION NUMBER: US/10/964,195  
; CURRENT FILING DATE: 2004-10-13  
; PRIOR APPLICATION NUMBER: US/09/320,156  
; PRIOR FILING DATE: 1999-05-26  
; PRIOR APPLICATION NUMBER: 08/404,499  
; PRIOR FILING DATE: 1995-03-17  
; NUMBER OF SEQ ID NOS: 14  
; SEQ ID NO 13  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Polypeptide encoded by the scFv23-gelonin immunotoxin  
US-10-964-195-13

Query Match 99.4%; Score 1269; DB 5; Length 498;  
Best Local Similarity 99.2%; Pred. No. 1.9e-114;  
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GLDTVSFSTKGATITTYVNFNLRLVKLKPGNSHGIPLLRKADDPGKAPVLVALSNDN 60  
Db 247 GLDTVSFSTKGATITTYVNFNLRLVKLKPGNSHGIPLLRKADDPGKAPVLVALSNDN 306  
Qy 61 GQLAEIAIDVTSVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120  
Db 307 GQLAEIAIDVTSVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 366  
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180  
Db 367 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 426  
Qy 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db 427 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 486  
Qy 241 ALLKFVDKDPK 251  
Db 487 ALLKFVDKDPK 497

RESULT 14  
US-10-074-596-11  
; Sequence 11, Application US/10074596  
; Publication No. US20030176331A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENBLUM, MICHAEL G.  
; APPLICANT: CHEUNG, LAWRENCE  
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF  
; FILE REFERENCE: MAKING THEOF  
; FILE REFERENCE: CLFR:007US  
; CURRENT APPLICATION NUMBER: US/10/074,596  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/268,402  
; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 507  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-074-596-11

Query Match 99.4%; Score 1269; DB 4; Length 507;  
Best Local Similarity 99.2%; Pred. No. 1.9e-114;  
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GLDTVSFSTKGATITTYVNFNLRLVKLKPGNSHGIPLLRKADDPGKAPVLVALSNDN 60  
Db 257 GLDTVSFSTKGATITTYVNFNLRLVKLKPGNSHGIPLLRKADDPGKAPVLVALSNDN 316  
Qy 61 GQLAEIAIDVTSVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 120  
Db 317 GQLAEIAIDVTSVVGQVQRNRSYFFKADPDAAYEGLFKNTIKTRLHFGSGYPSLSEGEK 376  
Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180  
Db 377 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 436  
Qy 181 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 240  
Db 437 FQORIRPANNTISLENKWKLSFQIRTSANGMFSEAVELERANGKYYVTVAVDQVKPKI 496  
Qy 241 ALLKFVDKDPK 251  
Db 497 ALLKFVDKDPK 507

RESULT 15  
US-09-765-527-259  
; Sequence 259, Application US/09765527  
; Patent No. US20020006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 259:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids



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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259

Query Match      99.1%; Score 1266; DB 3; Length 293;
Best Local Similarity 98.8%; Pred. No. 1.8e-114;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLDTVSFSTKGATITTYVNFLELRVKLKPEGNHGIPLLRKKADDPKAPVLVALSNDN 60
Db 23 GLDTVSFSTKGATITTYVNFLELRVKLKPEGNHGIPLLRKKADDPKAPVLVALSNDN 82

Qy 61 GOLAEIAIDVTSVTVVGVQVNRNSYFFPKADPAAYEGLEFKNTIKTRLHFGGSYPSEGEK 120
Db 83 GOLAEIAIDVTSVTVVGVQVNRNSYFFPKADPAAYEGLEFKNTIKTRLHFGGSYPSEGEK 142

Qy 121 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 180
Db 143 AYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNN 202

Qy 181 FQQRIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 240
Db 203 FQQRIRPANNTISLENKWKLSFOIRTSANGMFSEAVELERANGKYYVTAVDQVKPKI 262

Qy 241 ALLKFVDKDPK 251
Db 263 ALLKFVDKDPK 273
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Search completed: February 10, 2006, 10:44:48  
Job time : 164.937 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 10:39:04 ; Search time 12.9668 Seconds  
(without alignments)  
254.015 Million cell updates/sec

Title: US-10-717-243-101

Perfect score: 1277

Sequence: 1 GLDTVSFSTKGATYITVNF.....AVDQVKPALKLKFVDKDPK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pdb:\*
- 2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pdb:\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pdb:\*
- 4: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pdb:\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pdb:\*
- 6: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pdb:\*
- 7: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pdb:\*
- 8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	27.1	268	7	US-11-010-795-24
2	346	27.1	576	6	US-10-923-022-1
3	346	27.1	630	6	US-10-893-584-274
4	327	25.6	313	7	US-11-010-795-20
5	307	24.0	267	6	US-10-517-707A-1
6	248.5	19.5	200	6	US-10-923-022-10
7	246.5	19.3	190	6	US-10-923-022-11
8	245.5	19.2	198	6	US-10-923-022-3
9	245.5	19.2	199	6	US-10-923-022-7
10	245.5	19.2	198	6	US-10-923-022-5
11	243.5	19.1	188	6	US-10-923-022-4
12	243.5	19.1	188	6	US-10-923-022-8
13	243.5	19.1	189	6	US-10-923-022-6
14	240	18.8	267	6	US-10-517-707A-7
15	239	18.7	185	6	US-10-923-022-9
16	204	16.0	310	7	US-11-010-795-22
17	176.5	13.8	179	6	US-10-923-022-2
18	85.5	6.7	315	7	US-11-010-795-28
19	83	6.5	319	7	US-11-010-795-26
20	80.5	6.3	386	7	US-11-022-562-229
21	80.5	6.3	365	7	US-11-102-978-9
22	80.5	6.3	365	7	US-11-080-991-78
23	80.5	6.3	1088	7	US-11-098-686-10718
24	80	6.3	377	6	US-10-793-626-3014
25	80	6.3	459	6	US-10-453-372-1044

26	79	6.2	934	7	US-11-188-743-19	Sequence 19, Appl
27	79	6.2	934	7	US-11-183-294-20	Sequence 20, Appl
28	78.5	6.1	303	7	US-11-156-084-232	Sequence 232, App
29	78	6.1	951	6	US-10-453-372-1012	Sequence 1012, App
30	77.5	6.1	483	7	US-11-052-554A-107	Sequence 107, App
31	77	6.0	459	6	US-10-453-372-1018	Sequence 1018, App
32	77	6.0	459	6	US-10-453-372-1046	Sequence 1046, App
33	77	6.0	459	6	US-10-453-372-1048	Sequence 1048, App
34	77	6.0	459	6	US-10-453-372-1050	Sequence 1050, App
35	77	6.0	475	6	US-10-793-626-2076	Sequence 2076, App
36	77	6.0	627	6	US-10-873-528-191	Sequence 191, App
37	77	6.0	719	6	US-10-793-626-1548	Sequence 1548, App
38	77	6.0	947	6	US-10-453-372-1010	Sequence 1010, App
39	77	6.0	962	6	US-10-453-372-1042	Sequence 1042, App
40	76.5	6.0	417	6	US-10-995-561-791	Sequence 791, App
41	76.5	6.0	417	7	US-11-110-851-61	Sequence 61, Appl
42	75.5	5.9	1183	7	US-11-115-639-13	Sequence 13, Appl
43	75.5	5.9	1183	7	US-11-115-639-14	Sequence 14, Appl
44	75.5	5.9	1183	7	US-11-115-639-15	Sequence 15, Appl
45	75.5	5.9	1183	7	US-11-115-639-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-11-010-795-24  
; Sequence 24, Application US/11010795  
; Publication No. US20060005271A1  
; GENERAL INFORMATION:  
; APPLICANT: TUMER, NILGUN E.  
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE  
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS  
; FILE REFERENCE: OCIRS 3.0-085  
; CURRENT APPLICATION NUMBER: US/11/010,795  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: 60/529,348  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 24  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-11-010-795-24

Query Match	27.1%	Score 346;	DB 7;	Length 268;
Best Local Similarity	36.8%	Pred. No. 1e-24;		
Matches	93;	Conservative	45;	Mismatches 99; Indels 16; Gaps 9;
Qy	5	VSEFTKGATVITVVFNLNLRVLRKKEGN-SHGIPILRKKADDP-GKAFVLVALSNDNGQ	62	
Db	10	INFTTAGATVQSTTTFIRAVRGLTTGADVHRHIVLPNVRGLPQRFILVELSNHAEL	69	
Qy	63	LABIAIDVTSVYVGVQVRRNSYFFKADP-----AAEGLFKNTIKTR--LHFGGSYPS	115	
Db	70	SVTLALDVNAYVGVGRAGNSAYFFH--PDNQDAEAIHTLFTD-VQNRVTFAGGNYDR	126	
Qy	116	LEGEKA-YRETTDLGIEPIRIGIKLDENAIQKPTETIASLLVWQVMSAARFTFIE	174	
Db	127	LEQLAGLNRENIEGLNGPLEEASALSYVYSTGGTQLPTLARSFICICIMSEARFOYIE	186	
Qy	175	NQIRN-NFQOIRPANNITISLENKGLKLSFQRTSGANGMFSEAVLERANGKYYVTA	232	
Db	187	GENKTRIRYRNSAPDPSPVITLNSWGRSLTAIQESN-QGAFASPIQLORRNGSKFSYVD	245	
Qy	233	VDOVKPKIALKXF	245	
Db	246	VSILIPILALMWY	258	

RESULT 2

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; LENGTH: 630
; TYPE: PRT
; ORGANISM: Artificial Sequence

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Db      252 VDASGAKWVLVRDEIKPDVALLNVV 277

RESULT 5
US-10-517-707A-1
; Sequence 1, Application US/10517707A
; Publication No. US20060019885A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-134
; CURRENT APPLICATION NUMBER: US/10/517.707A
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06055
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: EP 02012911.0
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-707A-1

Query Match      24.0%; Score 307; DB 6; Length 267;
Best Local Similarity 36.3%; Pred. No. 4e-21;
Matches 89; Conservative 36; Mismatches 108; Indels 12; Gaps 7;

Qy      5 VSFSTKGATYITYVNFLELRVKLKPEGNHSHGIFLLRKKADDDPGKAFVLVALSNDNGQLA 64
Db      2 VSPRLSGATTSYGVFIKNLREALPYERKVNIFLLRSSISGSGR-YTLHLHTVYADETI 60

Qy      65 EIAIDVTSVYVVGQVNRNRSYFFKDA-PDAAYEGLFKNT-IKTLHFGGSYPSLE-GEKA 121
Db      61 SVAVDVNTVMYGLAGDSVYFFNEASATEAAKVFVKDAKKVTLPSYSGYERLQTAAGK 120

Qy      122 YRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQIRNPF 181
Db      121 IRENIPGLPALDSAI-----TTLUYTASGAASALLVLIQSTAESARYKPIEQOIGKRV 175

Qy      182 QORIRPANNTISLENKMGKLSFQIR-TSGANGMFSEAVELERANGKKYVVT--AVDQVKP 238
Db      176 DKTFLPSLATISLENNWSALSQIQLASTNNGQFESPVLIDGNNQRVSIINASARVTS 235

Qy      239 KIALL 243
Db      236 NIALL 240

RESULT 6
US-10-923-022-10
; Sequence 10, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis

US-10-923-022-10
; Sequence 11, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-11

Query Match      19.3%; Score 246.5; DB 6; Length 190;
Best Local Similarity 35.4%; Pred. No. 9.2e-16;
Matches 68; Conservative 31; Mismatches 74; Indels 19; Gaps 6;

Qy      5 VSFSTKGATYITYVNFLELRVKLKPEGNHSHGIFLLRKKADDDPGKAFVLVALSNDNGQLA 64
Db      10 INFETAGATVQSYTNFIRAVRGRLTVLPNVRGLPI-----NQRILVELSHAEISLV 61

Qy      65 EIAIDVTSVYVVGQVNRNRSYFFKADPD-----AAVEGLEFKNTIKTR--LHFGGSYPSLE 117
Db      62 TLALDVINA VVGVRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNRVYTFAGGNGYDRLE 118

Qy      118 GEKA-YRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQ 176
Db      119 QLAGNLRENIELGNGPLEEASALYYSTGGTQTLTARSFICIQMISEAARFQYIEG 178

Qy      177 IRNNFQQRIRPA 188
Db      179 MRTRIRYNRNSA 190

RESULT 7
US-10-923-022-11
; Sequence 11, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-11

Query Match      19.3%; Score 246.5; DB 6; Length 190;
Best Local Similarity 35.4%; Pred. No. 9.2e-16;
Matches 68; Conservative 31; Mismatches 74; Indels 19; Gaps 6;

Qy      5 VSFSTKGATYITYVNFLELRVKLKPEGNHSHGIFLLRKKADDDPGKAFVLVALSNDNGQLA 64
Db      10 INFETAGATVQSYTNFIRAVRGRLTVLPNVRGLPI-----NQRILVELSHAEISLV 61

Qy      65 EIAIDVTSVYVVGQVNRNRSYFFKADPD-----AAVEGLEFKNTIKTR--LHFGGSYPSLE 117
Db      62 TLALDVINA VVGVRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNRVYTFAGGNGYDRLE 118

Qy      118 GEKA-YRETTDLGIEPLRIGIKKLDENADNYKPTETIASLLVVIQMVSEAAARFTFIENQ 176
Db      119 QLAGNLRENIELGNGPLEEASALYYSTGGTQTLTARSFICIQMISEAARFQYIEG 178

Qy      177 IRNNFQQRIRPA 188
Db      179 MRTRIRYNRNSA 190

RESULT 8
US-10-923-022-3
; Sequence 3, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A

```

```

; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452USO (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-3

Query Match          19.2%; Score 245.5; DB 6; Length 198;
Best Local Similarity 37.0%; Pred. No. 1.2e-15;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

Qy 5 VSPSTKGATITYVNFNLELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ 62
Db 9 INFTTAGTQSYTNFIRAVRGLTTGADYRHEIPVLPNVRVGLPINQRFILVELSNHAEL 68
Qy 63 LAEIAIDVTSVVGVYQVRNSRPFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
Db 69 SVTILALDVTNAYVVGYSAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRVYTFAGGNYDR 125
Qy 116 LEGEKA-YRETTDGIPIRLIGIKKLDENALDNYKPTETIASSLLAVIOMYSEARFTFIE 174
Db 126 LEQAGNLRENIEUNGPLEEASALYYTSGTGQLPTLARSFFIICIMISEAARFOYIE 185
Qy 175 NQIRNNFQORIR 186
Db 186 GEMRT---RIR 193

RESULT 9
US-10-923-022-7
; Sequence 7, Application US/10923022
; Publication No. US20060005619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452USO (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-7

Query Match          19.2%; Score 245.5; DB 6; Length 198;
Best Local Similarity 37.0%; Pred. No. 1.2e-15;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

Qy 5 VSPSTKGATITYVNFNLELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ 62
Db 9 INFTTAGTQSYTNFIRAVRGLTTGADYRHEIPVLPNVRVGLPINQRFILVELSNHAEL 68
Qy 63 LAEIAIDVTSVVGVYQVRNSRPFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
Db 69 SVTILALDVTNAYVVGYSAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRVYTFAGGNYDR 125

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[illegible]

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; PRIOR FINDING DATES: 2002-02-27/
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-7

Query Match          19.2%   Score 245.5; DB 6; Length 198;
Best Local Similarity 37.0%; Pred. No. 1.2e-15;
Matches 71; Conservative 31; Mismatches 73; Indels 17; Gaps 8;

Qy      5 VSPSTKGATITVYNFNLNLRVKLKPGEN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ 62
       :.:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      9 INFTTAGTQVSNTFNFAVRGLTTGADVNRHEIPLVPINRVGLPIINQRFILVELSNHAEL 68
       :.:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      63 LAEIAIDVTSVYVGVOVRNSRPFKDAPD-----AAYEGLFKNKTIKTR--LHFGGSYPS 115
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Db      69 SVTIALDVNTWAVVGYGRAGNSAYFFH--PNQEDAEAITHLFTD-VGNRYTFAGFGNYDR 125
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; ORGANISM: Ricinus communis
US-10-923-022-4

Query Match      19.1%; Score 243.5; DB 6; Length 188;
Best Local Similarity 36.3%; Pred. No. 1.7e-15;
Matches 69; Conservative 30; Mismatches 68; Indels 23; Gaps 7;

Qy 5 VSPSTKGATYITYVNFNLRLVVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDNGOLA 64
Db 9 INFTTAGATVQSYTNFIRAVRGRLTVLPNVRGLPI-----NQRFILVELSNHAEISV 60

Qy 65 EIAIDVTSVYVGVQVNRNRSYFFKADP-----AAVEGLPKNTIKTR--LHFGGSYPSLE 117
Db 61 TLALDVTNAVYVGVGRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNYTFPAFGGNYDRLE 117

Qy 118 GEKA-VRETTDLGIEPLRIGIKKLDENAINDKYTEIASSLLVVIQMVSEARFTFIENQ 176
Db 118 QLAGNLRENIELGNGLPEEAISALYYSTGTQTLPLARSFIICIQMISEARFOYIEGE 177

Qy 177 IRNPFQORIR 186
Db 178 MRT-----RIR 183

RESULT 12
US-10-923-022-8
; Sequence 8, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452USO (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-8

Query Match      19.1%; Score 243.5; DB 6; Length 188;
Best Local Similarity 36.3%; Pred. No. 1.7e-15;
Matches 69; Conservative 30; Mismatches 68; Indels 23; Gaps 7;

Qy 5 VSPSTKGATYITYVNFNLRLVVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDNGOLA 64
Db 9 INFTTAGATVQSYTNFIRAVRGRLTVLPNVRGLPI-----NQRFILVELSNHAEISV 60

Qy 65 EIAIDVTSVYVGVQVNRNRSYFFKADP-----AAVEGLPKNTIKTR--LHFGGSYPSLE 117
Db 61 TLALDVTNAVYVGVGRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNYTFPAFGGNYDRLE 117

Qy 118 GEKA-VRETTDLGIEPLRIGIKKLDENAINDKYTEIASSLLVVIQMVSEARFTFIENQ 176
Db 118 QLAGNLRENIELGNGLPEEAISALYYSTGTQTLPLARSFIICIQMISEARFOYIEGE 177

Qy 177 IRNPFQORIR 186
Db 178 MRT-----RIR 183

RESULT 13
US-10-923-022-6
; Sequence 6, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452USO (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-6

Query Match      19.1%; Score 243.5; DB 6; Length 189;
Best Local Similarity 36.3%; Pred. No. 1.7e-15;
Matches 69; Conservative 30; Mismatches 68; Indels 23; Gaps 7;

Qy 5 VSPSTKGATYITYVNFNLRLVVKLPKGNHSHGIPLLRKADDPKAFVLVALSNDNGOLA 64
Db 10 INFTTAGATVQSYTNFIRAVRGRLTVLPNVRGLPI-----NQRFILVELSNHAEISV 61

Qy 65 EIAIDVTSVYVGVQVNRNRSYFFKADP-----AAVEGLPKNTIKTR--LHFGGSYPSLE 117
Db 62 TLALDVTNAVYVGVGRAGNSAYFFH--PDNQEDAEAIHTLFTD-VQNYTFPAFGGNYDRLE 118

Qy 118 GEKA-VRETTDLGIEPLRIGIKKLDENAINDKYTEIASSLLVVIQMVSEARFTFIENQ 176
Db 119 QLAGNLRENIELGNGLPEEAISALYYSTGTQTLPLARSFIICIQMISEARFOYIEGE 178

Qy 177 IRNPFQORIR 186
Db 179 MRT-----RIR 184

RESULT 14
US-10-517-707A-7
; Sequence 7, Application US/10517707A
; Publication No. US20060019885A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
; FILE REFERENCE: MER-134
; CURRENT APPLICATION NUMBER: US/10/517,707A
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06055
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: EP 02012911.0
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified byrodin 1 protein
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 48, 49, 51, 54
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Met, Ala, Gly, Pro, Ile
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Pro, Tyr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 55, 60, 64, 66
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; OTHER INFORMATION: Xaa=Thr, Ser
; OTHER INFORMATION: Xaa=Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 94, 95, 114
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, His, Asp, Glu, Asn, Gln, Lys,
; OTHER INFORMATION: Arg, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Pro, Ser, Thr, His, Lys
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 117, 119, 120, 121
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=His
; OTHER INFORMATION: Xaa=Ser
; OTHER INFORMATION: Xaa=Ala, Ser, thr, Pro, Asn, Asp, Glu, Gly, His,
; OTHER INFORMATION: Lys, Gln
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 122, 125, 139, 132
; OTHER INFORMATION: Xaa=Thr
; OTHER INFORMATION: Xaa=Ala, Pro
; OTHER INFORMATION: Xaa=Ala, Ile, Phe, Gly, Met, Pro, Val, Trp, Tyr
; OTHER INFORMATION: Xaa=Phe, Pro, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137) ... (143)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (152) ... (155)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ile, Met, Ser, Thr
; OTHER INFORMATION: Xaa=Ala, Gly, Pro
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Ser, Thr, His, Asp, Asn, Gln,
; OTHER INFORMATION: Lys, Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (187) ... (198)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Gln
; OTHER INFORMATION: Xaa=His, Lys, Arg, Asp, Glu, Asn,, Phe, Leu, Pro,
; OTHER INFORMATION: Ser, Tyr, Trp
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (200) ... (202)
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
; OTHER INFORMATION: Glu, Asn, Gln
; OTHER INFORMATION: Xaa=Asp
US-10-517-707A-7

Query Match 18.8%; Score 240; DB 6; Length 267;
Best Local Similarity 30.5%; Pred. No. 5.9e-15;
Matches 75; Conservative 33; Mismatches 124; Indels 14; Gaps 7;

Qy 5 VSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKKADDPGKAFVLVALSNDNGOLA 64
Db 2 VSPRLSGATTSTGYGFIKNLREALPYERKVNPILRRSSISGSR-YXXIXLTXKADETX 60

Qy 65 EIAIDVTSVYVGVQVNRNSYFFPKDA-PDAAYEGLFKWT-IKTRLHFGGSYPSLEGEKAY 122
Db 61 SVAXDXTNVYIMGVLAGDVSYFFNEASATEAAKXPKDAKKKXKTLPSYSGNY-----ERX 114

Qy 123 RETTDLGIEPLRIGIKLDENAIIDNYKPT--EIASLLVVIQMVSEAAARFTFIENQIRNN 180

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Db 115 QTXAXXXENKXPLGXPAKDSAXTTXXYXTASSAASAXXXIXQTAESARYKFIQQIGKR 174
Qy 181 FQORIRPANNNTISLENKWKLSFOIRTSGA-NGMFSEAVLELRANGKKYVVT--AVDOVK 237
Db 175 VDKTFLPSLATXSKENNSAXSXQXKASTNNGQFSPVVLIDGNNQORSITNASARVVT 234
Qy 238 PKIALL 243
Db 235 SNIALL 240

RESULT 15
US-10-923-022-9
; Sequence 9, Application US/10923022
; Publication No. US20060009619A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452USO (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/923,022
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/10/083,336
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-923-022-9

Query Match 18.7%; Score 239; DB 6; Length 185;
Best Local Similarity 36.3%; Pred. No. 4.4e-15;
Matches 69; Conservative 30; Mismatches 65; Indels 26; Gaps 8;

Qy 5 VSFSTKGATYTYVNFNLRLVKLPKGNHGIPLLRKKADDPGKAFVLVALSNDNGOLA 64
Db 9 INFRTAGATVQSYTNFIRAVRGLT---NRVGLPI-----NQRFILVELSNHAEISV 57

Qy 65 EIAIDVTSVYVGVQVNRNSYFFPKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPSLE 117
Db 58 TLALDVTNAYVGVYRAGNSAYFFH--PDNQEDAEATHLFTD-VQNRYYTAFGNGYDRLE 114

Qy 118 GERA-YRETTDLGIEPLRIGIKLDENAIIDNYKPTETIASLLVVIQMVSEAAARFTFIENQ 176
Db 115 QLAGNLARENIELGNGLPLEEALISALYYYSTGTGTQLPTLARSFIICIQMISEAARFQYIEGE 174

Qy 177 IRNNFOORIR 186
Db 175 MRT----RIR 180

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Search completed: February 10, 2006, 10:45:21  
Job time : 13.9668 secs